

jc580 U.S. PTO
05/28/99

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May 28, 1999

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jc503 U.S. PTO
09/322021
05/28/99

BOX PATENT APPLICATION

Assistant Commissioner
of Patents
Washington, D.C. 20231

Re: Application of Richard J. ARMITAGE,
William C. FANSLOW and Melanie K. SPRIGGS
entitled "MONOCLONAL ANTIBODIES TO CD40
LIGAND, PHARMACEUTICAL COMPOSITION
COMPRISING THE SAME AND HYBRIDOMAS
PRODUCING THE SAME" (As Amended)
Our Ref: A-7517

Dear Sir:

This is a request for a Continuation Application of pending prior Application No. 08/249,189 filed May 24, 1994, of Richard J. ARMITAGE, William C. FANSLOW and Melanie K. SPRIGGS entitled "MONOCLONAL ANTIBODIES TO CD40 LIGAND, PHARMACEUTICAL COMPOSITION COMPRISING THE SAME AND HYBRIDOMAS PRODUCING THE SAME" (now allowed); which in turn is a Continuation-In-Part of U.S. Application No. 07/969,703, filed October 23, 1992 (now abandoned); which in turn is a Continuation-In-Part of U.S. Application No. 07/805,723, filed December 5, 1991 (now abandoned); which in turn is a Continuation-In-Part of U.S. Application No. 07/783,707, filed October 25, 1991 (now abandoned).

This application is being filed under 37 C.F.R. § 1.53(b). Enclosed is a copy of the specification, claims and Abstract; and twenty-one (21) sheets of drawings. An executed Declaration and Power of Attorney will be submitted at a later date.

The prior application was assigned to Group Art Unit 1644.

Assistant Commissioner
of Patents

May 28, 1999
Page 2

A Preliminary Amendment, Information Disclosure Statement (accompanied by Form PTO-1449) and Statement in Support of Submission (accompanied by hard copy of Sequence Listing) are being simultaneously filed herewith.

The Government filing fee is calculated as follows:

| | | | | | | | | |
|-------------------------|----------|------|---|----------|---|---------|---|-------------------------|
| Total claims | <u>3</u> | - 20 | = | <u>0</u> | X | \$18.00 | = | <u>\$0.00</u> |
| Independent | | | | | | | | |
| claims | <u>2</u> | - 3 | = | <u>0</u> | X | \$78.00 | = | <u>\$0.00</u> |
| Base Fee | | | | | | | | <u>\$ 760.00</u> |
| TOTAL FILING FEE | | | | | | | | <u>\$ 760.00</u> |

A check for the statutory fee of \$760.00 is attached. The Assistant Commissioner is directed and authorized to charge or credit any difference or overpayment to Deposit Account No. 19-4880. The Assistant Commissioner is also hereby authorized to charge any fees under 37 C.F.R. § 1.16 and § 1.17 which may be required during the entire pendency of the application to Deposit Account No. 19-4880. A duplicate copy of this transmittal letter is attached.

Respectfully submitted,

SUGHRUE, MION, ZINN,
MACPEAK & SEAS, PLLC
Attorneys for Applicant

By


Gordon Kit

Registration No. 30,764

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

RICHARD ARMITAGE et al

Cont. of
Appln. No.: 08/249,189

Group Art Unit: 1644

Filed: May 28, 1999

Examiner: Gambel, P.

For: MONOCLONAL ANTIBODIES TO CD40 LIGAND,
PHARMACEUTICAL COMPOSITION COMPRISING
THE SAME AND HYBRIDOMAS PRODUCING THE
SAME (As Amended)

PRELIMINARY AMENDMENT

Assistant Commissioner
for Patents
Washington, D.C. 20231

Sir:

Prior to examining to the above-identified application,
please amend the application as follows.

IN THE TITLE:

Please delete the present title of the above-identified
application, and insert therefor

-- MONOCLONAL ANTIBODIES TO CD40 LIGAND,
PHARMACEUTICAL COMPOSITION COMPRISING
THE SAME AND HYBRIDOMAS PRODUCING THE SAME --.

IN THE SPECIFICATION:

Please amend the specification as follows:

Page 1, lines 7-10, delete in their entirety, and insert therefor

-- This application is a Continuation of Application Serial No. 08/249,189, filed May 24, 1994 (now allowed); which in turn is a Continuation-In-Part of Application Serial No. 07/969,703, filed October 23, 1992 (now abandoned); which in turn is a Continuation-In-Part of Application Serial No. 07/805,723, filed December 5, 1991 (now abandoned); which in turn is a Continuation-In-Part of Application Serial No. 07/783,707, filed October 25, 1991 (now abandoned). --.

Page 3, line 37, change "Figure 1 illustrates" to -- Figure 1 (SEQ ID NO:1 and SEQ ID NO:2) illustrates --.

Page 4, line 4, change "Figure 2 illustrates" to -- Figure 2 (SEQ ID NO:11 and SEQ ID NO:12) illustrates --;

line 10, after "human", insert -- (SEQ ID NO:12) --;

line 10, after "murine", insert -- (SEQ ID NO:2) --;

and

line 12, change "Figure 4 illustrates" to -- Figures 4A-4B illustrate --.

Page 5, line 1, change "Figure 13 illustrates" to -- Figures 13A-13B illustrate --;

line 4, change "Figure 14 shows" to -- Figures 14A-14B show --;

line 7, change "Figure 15 shows representative" to -- Figures 15A-15D show representative --;

line 11, change "Figure 16 illustrates" to -- Figures 16A-16D illustrate --; and

PRELIMINARY AMENDMENT
Cont. of USSN 08/249,189

line 20, change "Figure 19 illustrates" to
-- Figure 19A-19B illustrate --.

Page 18, line 9, change "Np40" to -- NP40 --.

Page 33, line 9, change "Figure 13 compares" to
-- Figures 13A-13B compare --.

Page 36, line 43, change "Figure 14" to
-- Figures 14A-14B --; and

Page 37, line 1, change "Figure 14" to -- Figures 14A-14B --;
and

line 16, change "acid 50" to -- acid 51 --.

Page 38, line 22, change "acid 50" to -- acid 51 --.

Page 43, line 11, after "Sepharose", insert -- ® --; and

line 13, after "Sepharose", insert -- ® --.

Page 44, in Table 9 (number 3), after "Sepharose", insert
-- ® --.

Page 45, line 22, change "Figure 15" to
-- Figures 15A-15D --.

Page 46, line 3, change "Figure 16" to -- Figures 16A-16D --;
line 17, change "(designated M90 and M91)" to
-- (designated hCD40L-M90 and hCD40L-M91) --;

line 19, after "Collection", insert
-- 12301 Parklawn Drive, Rockville, MD 20852, USA --;

line 19, change "on _____," to -- on
February 23, 1996, --; and

line 20, change "_____ (M90) and _____ (M91)" to
-- HB-1205 (hCD40L-M90) and HB-12056 (hCD40L-M91) --.

Page 47, line 5, change "Figures 18 and 19" to -- Figures 18
and 19A-19B --.

PRELIMINARY AMENDMENT
Cont. of USSN 08/249,189

IN THE CLAIMS:

Please cancel Claims 1-27.

Please add the following new claims:

-- Claim 28. A monoclonal antibody that binds to mouse CD40L encoded by vector pDC406-mCD40-L having ATCC Accession No. 68872.

Claim 29. A pharmaceutical composition comprising a monoclonal antibody according to Claim 28, and a pharmaceutically acceptable carrier.

Claim 30. A hybridoma which secretes a monoclonal antibody that binds to mouse CD40L encoded by vector pDC406-mCD40-L having ATCC Accession No. 68872. --

REMARKS

The title has been amended consistent with the claims of the present application.

The specification has been amended for purposes of clarification and to correct obvious typographical errors therein. Support for the amendment regarding pages 37-38 can be found, *inter alia*, in SEQ ID NOs: 15 and 20. The amendments to the specification are essentially identical to those made in parent application Serial No. 08/249,189 (now allowed).

An ATCC deposit receipt for the hybridomas described in the specification is attached hereto.

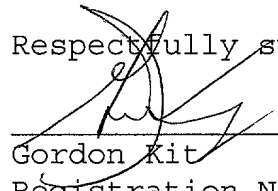
New Claims 28-30 have been added to more clearly recite the invention of interest. Support for new Claims 28-30 can be found in, *inter alia*, the cancelled Claims, and Examples 4 and 7 provided in the present specification.

PRELIMINARY AMENDMENT
Cont. of USSN 08/249,189

Hence, the amendments to the specification, and new Claims 28-30 do not constitute new matter, and thus entry is requested.

The Examiner is invited to contact the undersigned at the below listed number on any questions which might arise.

Respectfully submitted,



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Date: May 28, 1999

TITLE

NOVEL CYTOKINE THAT BINDS CD40

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation-in-part application of United States Patent Application 07/969,703, filed October 23, 1992, which is a continuation-in-part of United States Patent Application 07/805,723, filed on December 5, 1991, which is a continuation-in-part of United States Patent Application 07/783,707, filed on October 25, 1991.

TECHNICAL FIELD OF THE INVENTION

The present invention relates to a novel cytokine. More specifically, the present invention relates to the cloning of a murine and a human cytokine that binds to a human CD40 having both agonist and antagonist activity in soluble and membrane-bound forms.

BACKGROUND OF THE INVENTION

Cytokines that have an "Interleukin" designation are those protein factors that influence immune effector cells. Cytokines designated interleukin-1 through interleukin-12 have been reported and named as an interleukin. Other known cytokines include tumor necrosis factor (TNF), granulocyte-macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), mast cell growth factor (MGF), epidermal growth factor (EGF), platelet-derived growth factor (PDGF), nerve growth factor (NGF), erythropoietin (EPO), γ -interferon (γ -IFN) and others.

DNAs for two different TNF receptors (Type I and Type II) have been cloned (Smith et al., *Science* 248:1019, 1990; and Schall et al., *Cell* 61:361, 1990). Both forms of TNF receptor are related to each other and belong to a family of receptors whose members include nerve growth factor receptor (Johnson et al., *Cell* 47:545, 1986), B cell antigen CD40 (Stamenkovic et al., *EMBO J.* 8:1403, 1989), T cell antigen OX40 (Mallett et al., *EMBO J.* 9:1063, 1990), human *Fas* antigen (Itoh et al., *Cell* 66:233, 1991) and murine 4-1BB receptor (Kwon et al., *Cell. Immunol.* 121:414, 1989 [Kwon et al. I] and Kwon et al., *Proc. Natl. Acad. Sci. USA* 86:1963, 1989 [Kwon et al. II]).

Human CD40 protein (CD40) is a peptide of 277 amino acids having a molecular weight of 30,600, and a 19 amino acid secretory signal peptide comprising predominantly hydrophobic amino acids (Stamenkovic et al.). The molecular weight (exclusive of glycosylation) of the mature human CD40 protein is 28,300. A cDNA encoding human CD40 was isolated from a cDNA library prepared from Burkitt lymphoma cell line Raji. The putative protein encoded by the CD40 cDNA contains a putative leader sequence, trans-membrane domain and a number of other features common to membrane-bound receptor proteins. CD40

has been found to be expressed on B lymphocytes, epithelial cells and some carcinoma cell lines.

A monoclonal antibody (mAb) directed against CD40 has been shown to mediate various functional effects of human B cells. These effects include: (a) homotypic adhesions (Gordon et al., *J. Immunol.* 140:1425, 1988 [Gordon et al. I]); (b) increased cell size (Gordon et al. I and Valle et al., *Eur. J. Immunol.* 19:1463, 1989); (c) proliferation of B cells activated with anti-IgM, anti-CD20 mAb, phorbol ester alone (Clark et al., *Proc. Natl. Acad. Sci. USA* 83:4494, 1986; and Paulie et al., *J. Immunol.* 142:590, 1989), or phorbol ester combined with interleukin-4 (Gordon et al., *Eur. J. Immunol.* 17:1535, 1987 [Gordon et al. II]; and (d) production of IgE (Jabara et al., *J. Exp. Med.* 172:1861, 1990; Zhang et al., *J. Immunol.* 146:1836, 1991) and IgM (Gascan et al., *J. Immunol.* 147:8, 1991) from interleukin-4 (IL-4) stimulated T-depleted cultures.

One such antibody, called mAb 89 by Banchereau et al., *Clin. Immunol. Spectrum* 3:8, 1991 [Banchereau et al. I], was found to induce human B cell proliferation at a relatively low antibody concentration (30 ng/ml or about 10^{-10} M). Proliferation lasted two to three weeks and resulted in a ten-fold expansion of the human B cell population. Optimal stimulation of the B cells occurred when CD40 surface molecule was cross-linked by IgM. Fab fragments of another anti-CD40 mAb induced only a weak proliferative response. Further, Banchereau et al., *Science* 251:70, 1991 [Banchereau et al. II] reported that resting human B cells entered a state of sustained proliferation when incubated with both a murine fibroblastic Ltk⁻ cell line that was transfected with human Fc receptor and with a monoclonal antibody specific for human CD40. Banchereau et al. II found that cross-linking CD40 is necessary for clonal expansion of B cells.

CD23 is a low affinity IgE receptor that has been found to be expressed on most IgM⁻/IgD⁻ mature B cells, but not T cells. CD23 has been sequenced and its sequence was described in Kikutani et al., *Cell* 47:657, 1986. Soluble CD23 (sCD23) was found to induce a pyrogenic reaction in rabbits and this reaction was abrogated by administration of human IgE (Ghaderi et al., *Immunology* 73:510, 1991). Therefore, CD23 may be an appropriate marker for soluble CD40 or CD40-L effects.

Prior to the present invention, a ligand for CD40 was unknown. Accordingly, there is a need in the art to identify and characterize a CD40 ligand (CD40-L).

SUMMARY OF THE INVENTION

A novel cytokine, hereafter referred to as "CD40-L," has been isolated and characterized. The nucleotide sequence and deduced amino acid sequence of representative murine CD40-L cDNA is disclosed in SEQ ID NO:1 and Figure 1, and the amino acid sequence is also listed in SEQ ID NO:2. The nucleotide sequence and deduced amino acid sequence of representative human CD40-L cDNA is disclosed in SEQ ID NO:11 and Figure 2, and the amino acid sequence is also listed in SEQ ID NO:12. The present invention further

comprises other CD40-L polypeptides encoded by nucleotide sequences that hybridize, under moderate or severe stringency conditions, to probes defined by SEQ ID NO:11 (the coding region of human CD40-L), fragments of the sequence extending from nucleotide 46 to nucleotide 828 of SEQ ID NO:11, or to DNA or RNA sequences complementary to Figure 2 (SEQ ID NO:11) or fragments thereof. The invention further comprises nucleic acid sequences which, due to the degeneracy of the genetic code, encode polypeptides substantially identical or substantially similar to polypeptides encoded by the nucleic acid sequences described above, and sequences complementary to them.

CD40-L is a type II membrane polypeptide having an extracellular region at its C-terminus, a transmembrane region and an intracellular region at its N-terminus. A soluble version of murine CD40-L has been found in supernatants from EL-4 cells and EL-4 cells sorted on the basis of a biotinylated CD40/Fc fusion protein described herein. Soluble CD40-L comprises an extracellular region of CD40-L or a fragment thereof. The protein sequence of murine CD40-L is described in Figure 1 and SEQ ID NO:2, and human CD40-L in Figure 2 and SEQ ID NO:12. The extracellular region of murine CD40-L extends from amino acid 47 to amino acid 260 in Figure 1 and SEQ ID NO:2, and of human CD40-L from amino acid 47 to amino acid 261 in Figure 2 and SEQ ID NO:12. CD40-L biological activity is mediated by binding of this cytokine with CD40 and includes B cell proliferation and induction of antibody secretion, including IgE secretion.

The present invention further provides antisense or sense oligonucleotides (deoxyribonucleotides or ribonucleotides) that correspond to a sequence of at least about 12 nucleotides selected from the nucleotide sequence of CD40-L or DNA or RNA sequences complementary to the nucleotide sequence of CD40-L as described in SEQ ID NO:1 and SEQ ID NO:11 and in Figures 1 and 2. Such antisense or sense oligonucleotides prevent transcription or translation of CD40-L mRNA or polypeptides.

Further still, the present invention provides CD40-L peptide fragments that correspond to a protein sequence of at least 10 amino acids selected from the amino acid sequence encoded by SEQ ID NO:1 or SEQ ID NO:11 that can act as immunogens to generate antibodies specific to the CD40-L immunogens. Such CD40-L immunogen fragments can serve as antigenic determinants in providing monoclonal antibodies specific for CD40-L.

The invention also provides a human CD40/Fc fusion protein and a soluble CD40 protein (sCD40) comprising the extracellular region of human CD40. Both sCD40 and CD40/Fc fusion protein can inhibit CD40-L or anti-CD40 mAb induced B cell stimulation, IL-4-induced IgE stimulation and IL-4 induced CD23 induction in B cells.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates nucleotide and amino acid sequences corresponding to murine CD40-L. This protein is a type II polypeptide having its N-terminus as its intracellular domain, followed by a transmembrane region, and an extracellular domain at the C-terminus of the

polypeptide. The extracellular domain, which is longer than either the intracellular domain or the transmembrane region, contains one potential N-linked glycosylation site and two potential disulfide bonds in view of four cysteine (Cys) residues.

Figure 2 illustrates nucleotide and amino acid sequences corresponding to human CD40-L. This protein is a type II polypeptide having its N-terminus as its intracellular domain, followed by a transmembrane region, and an extracellular domain at the C-terminus of the polypeptide. The extracellular domain, which is longer than either the intracellular domain or the transmembrane region, contains 1 potential N-linked glycosylation site and 2 potential disulfide bonds in view of 5 cysteine (Cys) residues.

Figure 3 illustrates a comparison of protein sequences of human and murine CD40-L showing 77.7% homology at the amino acid level.

Figure 4 illustrates proliferation of T cell depleted human peripheral blood mononuclear cells (PBMC) caused by incubation with CV1 cells transfected with full length murine CD40-L cDNA (SEQ ID NO:1) and expressing bound CD40-L (CD40-L⁺CV1 cells) when compared with CV1 cells transfected with empty vector (HAVEO) and not expressing bound murine CD40-L. The day 7 proliferation results show that CD40-L⁺CV1 cells significantly increase proliferation of T- cell depleted PBMC in the presence or absence of interleukin-4 (IL-4).

Figure 5 illustrates a second determination of T cell depleted PBMC proliferation with addition of bound murine CD40-L and 10 ng/ml of IL-4. These data show no co-mitogenic effect of IL-4 but continued strong mitogenic effect of bound CD40-L.

Figure 6 illustrates that bound CD40-L augments IgE secretion.

Figure 7 illustrates that membrane-bound CD40-L stimulates CD23 shedding in the presence of IL-4.

Figure 8 illustrates proliferation of murine splenic B cells caused by membrane-bound murine CD40-L or 7A1 cells, which is a helper T cell clone.

Figure 9 illustrates a comparison of murine EL40.9 cells, a sorted cell line that was sorted on the basis of expression of murine CD40-L and T cells 7A1 for induction of an antigen-specific response indicated by plaque forming cells (PFC) by anti-sheep red blood cells (SCBC).

Figure 10 illustrates a comparison of B cell proliferative activity of membrane-bound CD40-L and other cell types transfected with different cDNAs. Membrane-bound CD40-L showed significantly more B cell proliferative activity than a helper T cell clone or other control cells.

Figure 11 illustrates that 7C2 cells (a helper T cell clone) and CV1 cells transfected with murine CD40-L cDNA induce anti SRBC plaque forming cells.

Figure 12 illustrates a comparison of two helper T cell clones with cells expressing membrane-bound CD40-L for inducing murine B cell proliferation.

Figure 13 illustrates induction of antigen-specific plaque forming cells by membrane-bound CD40-L and a helper T cell clone in the presence or absence of added interleukin-2 (IL-2).

Figure 14 shows effects of membrane-bound CD40-L stimulating B cell proliferation and IgE secretion. The effects of membrane-bound CD40-L were inhibited by CD40 receptor but not by TNF receptor.

Figure 15 shows representative FACS profiles of peripheral blood T cells stimulated for 16 hours with 10 ng/ml PMA and 500 ng/ml ionomycin, and stained with 5 µg/ml CD40/Fc, a control Fc protein, IL-4 receptor/Fc, murine IgG₁, and a CD40-L monoclonal antibody referred to as M90.

Figure 16 illustrates the ability of monoclonal antibodies M90 and M91 to inhibit binding of 2µg/ml CD40/Fc to peripheral blood T cells activated as described for Figure 15.

Figure 17 demonstrates the ability of anti-CD40-L monoclonal antibodies to bind trimeric CD40-L and inhibit the ability of CD40-L to induce B cell proliferation. Purified tonsil B cells were cultured with 5 µg/ml immobilized rabbit anti-human IgM and recombinant soluble human CD40-L. M90, M91 or an isotype control antibody were titrated into the cultures; incorporation of tritiated thymidine was used as a measure of proliferation.

Figure 18 presents the binding of trimeric human and murine CD40-L and dimeric human and murine CD40-L to C40/Fc as determined in a biosensor assay.

Figure 19 illustrates the binding of trimeric human CD40-L and two preparations of monomeric human CD40-L to C40/Fc as determined in a biosensor assay.

DETAILED DESCRIPTION OF THE INVENTION

Novel polypeptides that can act as a ligand for murine and human CD40 have been isolated and sequenced. More particularly, cDNAs encoding these ligands have been cloned and sequenced. Further provided are methods for expression of recombinant CD40-L polypeptides. CD40-L polypeptide include other forms of mammalian CD40-L, such as derivatives or analogs of human or murine CD40-L. Murine and human CD40-L comprise a 214 and 215, respectively amino acid extracellular region at the C-terminus of full length, membrane-bound polypeptide. The extracellular region contains the domain that binds to CD40. Murine and human CD40-L further comprise a homologous hydrophobic 24 amino acid transmembrane region delineated by charged amino acids on either side and a 22 amino acid intracellular region at their N-termini. The present invention further comprises full length CD40-L polypeptides or fragments thereof comprising all or part of the extracellular region or derivatives of the extracellular region and mammalian cells transfected with a cDNA encoding murine or human CD40-L and expressing human or murine CD40-L as a membrane-bound protein.

The present invention comprises isolated DNA sequences encoding CD40-L polypeptides and DNA or RNA sequences complementary to such isolated DNA sequences.

The isolated DNA sequences and their complements are selected from the group consisting of (a) nucleotides 184 through 828, 193 through 828, 193 through 762, or 403 through 762 of the DNA sequence set forth in Figure 2 (SEQ ID NO:11) and their complements, (b) DNA sequences which hybridize to the DNA sequences of (a) or their complements under conditions of moderate stringency and which encode a CD40-L polypeptide, analogs or derivatives thereof, and (c) DNA sequences which, due to the degeneracy of the genetic code, encode CD40-L polypeptides encoded by any of the foregoing DNA sequences and their complements. In addition, the present invention includes vectors comprising DNA sequences encoding CD40-L polypeptides and analogs, and host cells transfected with such vectors.

The novel cytokine disclosed herein is a ligand for CD40, a receptor that is a member of the TNF receptor super family. Therefore, CD40-L is likely to be responsible for transducing signal via CD40, which is known to be expressed, for example, by B lymphocytes. Full-length CD40-L is a membrane-bound polypeptide with an extracellular region at its C terminus, a transmembrane region, and an intracellular region at its N-terminus. A soluble version of CD40-L can be made from the extracellular region or a fragment thereof and a soluble CD40-L has been found in culture supernatants from cells that express a membrane-bound version of CD40-L. The protein sequence of the extracellular region of murine CD40-L extends from amino acid 47 to amino acid 260 in Figure 1 and SEQ ID NO:2. The protein sequence of the extracellular region of human CD40-L extends from amino acid 47 to amino acid 261 in Figure 2 and SEQ ID NO:12. The biological activity of CD40-L is mediated by binding to CD40 or a species-specific homolog thereof and comprises proliferation of B cells and induction of immunoglobulin secretion from activated B cells. CD40-L (including soluble monomeric and oligomeric forms, as well as membrane-bound forms) can effect B cell proliferation and immunoglobulin secretion (except IgE secretion) without the presence of added IL-4, in contrast to anti-CD40 antibodies, which require IL-4 and cross-linking to mediate activity.

CD40-L refers to a genus of polypeptides which are capable of binding CD40, or mammalian homologs of CD40. As used herein, the term "CD40-L" includes soluble CD40-L polypeptides lacking transmembrane and intracellular regions, mammalian homologs of human CD40-L, analogs of human or murine CD40-L or derivatives of human or murine CD40-L.

CD40-L may also be obtained by mutations of nucleotide sequences coding for a CD40-L polypeptide. A CD40-L analog, as referred to herein, is a polypeptide substantially homologous to a sequence of human or murine CD40-L but which has an amino acid sequence different from native sequence CD40-L (human or murine species) polypeptide because of one or a plurality of deletions, insertions or substitutions. Analogs of CD40-L can be synthesized from DNA constructs prepared by oligonucleotide synthesis and ligation or by site-specific mutagenesis techniques.

The primary amino acid structure of human or murine CD40-L may be modified to create CD40-L derivatives by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like, or by creating

amino acid sequence mutants. Covalent derivatives of CD40-L are prepared by linking particular functional groups to CD40-L amino acid side chains or at the N-terminus or C-terminus of a CD40-L polypeptide or the extracellular domain thereof. Other derivatives of CD40-L within the scope of this invention include covalent or aggregative conjugates of CD40-L or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. For example, the conjugate may comprise a signal or leader polypeptide sequence at the N-terminal region or C-terminal region of a CD40-L polypeptide which co-translationally or post-translationally directs transfer of the conjugate from its site of synthesis to a site inside or outside of the cell membrane or cell wall (e.g. the α -factor leader of *Saccharomyces*). CD40-L polypeptide fusions can comprise polypeptides added to facilitate purification and identification of CD40-L (e.g. poly-His), or fusions with other cytokines to provide novel polyfunctional entities. Other cytokines include, for example, any of interleukins-1 through 13, TNF (tumor necrosis factor), GM-CSF (granulocyte macrophage-colony stimulating factor), G-CSF (granulocyte-colony stimulating factor), MGF (mast cell growth factor), EGF (epidermal growth factor), PDGF (platelet-derived growth factor), NGF (nerve growth factor), EPO (erythropoietin), γ -IFN (gamma interferon), 4-1BB-L (4-1BB ligand) and other cytokines that affect immune cell growth, differentiation or function.

Nucleic acid sequences within the scope of the present invention include DNA and/or RNA sequences that hybridize to the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:11 or the complementary strands, under conditions of moderate or severe stringency. Moderate stringency hybridization conditions refer to conditions described in, for example, Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1, pp. 1.101-104, Cold Spring Harbor Laboratory Press, (1989). Conditions of moderate stringency, as defined by Sambrook et al., include use of a prewashing solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0) and hybridization conditions of 50°C, 5 X SSC, overnight. Conditions of severe stringency include higher temperatures of hybridization and washing.

Biological activity of CD40-L may be determined, for example, by competition for binding to the ligand binding domain of CD40 (i.e. competitive binding assays). Both murine CD40-L and human CD40-L bind to human CD40. The binding affinity of murine CD40-L (expressed on sorted murine EL-40.9 cells) for human CD40 was approximately $1.74 \times 10^9 \text{ M}^{-1}$. Similarly, the binding affinity of murine CD40-L (expressed on unsorted murine EL-46.1 cells) for human CD40 was approximately $2.3 \times 10^9 \text{ M}^{-1}$. Both binding affinity measurements are within a range typical of cytokine/cytokine receptor binding.

One configuration of a competitive binding assay for CD40-L polypeptide uses a radiolabeled, soluble murine CD40-L according to Figure 1 (SEQ ID NO:1) or human CD40-L according to Figure 2 (SEQ ID NO:11), and intact cells expressing CD40 (e.g., human B cells). Instead of intact cells, one could substitute soluble CD40 (such as a CD40/Fc fusion protein) bound to a solid phase through a Protein A or Protein G interaction with the Fc region

of the fusion protein. A second configuration of a competitive binding assay utilizes radiolabeled soluble CD40 such as a CD40/Fc fusion protein, and intact cells expressing CD40-L. Alternatively, soluble CD40-L could be bound to a solid phase.

Competitive binding assays can be performed using standard methodology. For example, radiolabeled murine CD40-L can be used to compete with a putative CD40-L homolog to assay for binding activity against surface-bound CD40. Qualitative results can be obtained by competitive autoradiographic plate binding assays, or Scatchard plots may be utilized to generate quantitative results.

Competitive binding assays with intact cells expressing CD40 can be performed by two methods. In a first method, B cells are grown either in suspension or by adherence to tissue culture plates. Adherent cells can be removed by treatment with 5 mM EDTA treatment for ten minutes at 37° C. In a second method, transfected COS cells expressing membrane-bound CD40 can be used. COS cells or another mammalian cell can be transfected with human CD40 cDNA in an appropriate vector to express full length CD40 with an extracellular region exterior to the cell.

Alternatively, soluble CD40 can be bound to a solid phase such as a column chromatography matrix, or a tube or similar substrate suitable for analysis for the presence of a detectable moiety such as ¹²⁵I. Binding to a solid phase can be accomplished, for example, by obtaining a CD40/Fc fusion protein and binding it to a protein A or protein G surface.

Another means to measure the biological activity of CD40-L and homologs thereof is to utilize conjugated, soluble CD40 (for example, ¹²⁵I-CD40/Fc) in competition assays similar to those described above. In this case, however, intact cells expressing CD40-L, or soluble CD40-L bound to a solid substrate, are used to measure competition for binding of conjugated, soluble CD40 to CD40-L by a sample containing a putative CD40 homolog.

CD40-L may also be assayed by measuring biological activity in a B cell proliferation assay. Human B cells may be obtained from human tonsils by purification by negative selection and Percoll density sedimentation, as described by Defrance et al., *J. Immunol.* 139:1135, 1987. Burkitt lymphoma cell lines may be used to measure cell proliferation in response to CD40-L. Examples of Burkitt lymphoma cell lines include, for example, Raji (ATCC CCL 86), Daudi (ATCC CCL 213) and Namalwa (ATCC CRL 1432). Membrane-bound CD40-L stimulated B cell proliferation. Oligomeric, preferably dimeric, CD40-L can stimulate B cell proliferation. CD40 (receptor) antagonizes CD40-L proliferation of B cells.

Yet another assay for determining CD40-L biological activity is to measure immunoglobulin produced by B cells in response to activation by CD40-L or a derivative or analog thereof. Polyclonal immunoglobulin secretion can be measured, for example, by incubating with 5 x 10⁵ B cells/ml in culture for at least seven days. Immunoglobulin (Ig) production can be measured by an ELISA assay such as one described in Maliszewski et al., *J. Immunol.* 144:3028, 1990 [Maliszewski et al. I] or Maliszewski et al., *Eur J. Immunol.* 20:1735, 1990 [Maliszewski et al. II]. Murine B cells can be obtained, for example, from mice

and cultured according to procedures described in Grabstein et al., *J. Exp. Med.* 163:1405, 1986 [Grabstein et al. I], Maliszewski et al. I, and Maliszewski et al. II.

CD40-L can be used in a binding assay to detect cells expressing CD40. For example, murine CD40-L according to Figure 1 (SEQ ID NO:1) or human CD40-L according to Figure 2 (SEQ ID NO:11), or an extracellular domain or a fragment thereof, can be conjugated to a detectable moiety such as ^{125}I . Radiolabeling with ^{125}I can be performed by any of several standard methodologies that yield a functional ^{125}I -CD40-L molecule labeled to high specific activity. Alternatively, another detectable moiety such as an enzyme that can catalyze a colorimetric or fluorometric reaction, biotin or avidin may be used. Cells expressing CD40 can be contacted with conjugated CD40-L. After incubation, unbound conjugated CD40-L is removed and binding is measured using the detectable moiety.

CD40-L polypeptides may exist as oligomers, such as dimers or trimers. Oligomers are linked by disulfide bonds formed between cysteine residues on different CD40-L polypeptides. Alternatively, one can link two soluble CD40-L domains with a Gly₄SerGly₅Ser linker sequence, or other linker sequence described in United States Patent 5,073,627, which is incorporated by reference herein. CD40-L polypeptides may also be created by fusion of the C terminal of soluble CD40-L (extracellular domain) to the Fc region of IgG1 (for example, SEQ ID NO:3) as described for the CD40/Fc fusion protein. CD40-L/Fc fusion proteins are allowed to assemble much like heavy chains of an antibody molecule to form divalent CD40-L. If fusion proteins are made with both heavy and light chains of an antibody, it is possible to form a CD40-L oligomer with as many as four CD40-L extracellular regions.

Fusion proteins can be prepared using conventional techniques of enzyme cutting and ligation of fragments from desired sequences. PCR techniques employing synthetic oligonucleotides may be used to prepare and/or amplify the desired fragments. Overlapping synthetic oligonucleotides representing the desired sequences can also be used to prepare DNA constructs encoding fusion proteins. Fusion proteins can also comprise CD40-L and two or more additional sequences, including a leader (or signal peptide) sequence, Fc region, linker sequence, and sequences encoding highly antigenic moieties that provide a means for facile purification or rapid detection of a fusion protein.

Signal peptides facilitate secretion of proteins from cells. An exemplary signal peptide is the amino terminal 25 amino acids of the leader sequence of human interleukin-7 (IL-7; Goodwin et al., *Proc. Natl. Acad. Sci. U.S.A.* 86:302, 1989; Figure 2B). Other signal peptides may also be employed. For example, certain nucleotides in the IL-7 leader sequence can be altered without altering the amino acid sequence. Additionally, amino acid changes that do not affect the ability of the IL-7 sequence to act as a leader sequence can be made.

The Flag[®] octapeptide (Asp-Tyr-Lys-Asp-Asp-Asp-Lys) does not alter the biological activity of fusion proteins, is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid detection and facile purification of the

expressed fusion protein. The Flag[®] sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing, fusion proteins capped with this peptide may also be resistant to intracellular degradation in *E. coli*. A murine monoclonal antibody that binds the Flag[®] sequence has been deposited with the ATCC under accession number HB 9259; methods of using the antibody in purification of fusion proteins comprising the Flag[®] sequence are described in U.S. Patent 5,011,912, which is incorporated by reference herein.

Suitable Fc regions are defined as Fc regions that can bind to protein A or protein G, or alternatively, are recognized by an antibody that can be used in purification or detection of a fusion protein comprising the Fc region. Preferable Fc regions include the Fc region of human IgG₁ or murine IgG₁. One example is the human IgG₁ Fc region shown in SEQ ID NO:3; another example is an Fc region encoded by cDNA obtained by PCR from oligonucleotide primers from SEQ ID NO:9 and SEQ ID NO:10 with human cDNA as a template. Portions of a suitable Fc region may also be used, for example, an Fc region of human IgG₁ from which has been deleted a sequence of amino acids responsible for binding to protein A, such that the resultant Fc region binds to protein G but not protein A.

The [Gly₄Ser]₃ repeat sequence provides a linker sequence that separates the extracellular region of the CD40-L from the Fc portion of the fusion protein by a distance sufficient to ensure that the CD40-L properly folds into its secondary and tertiary structures. Suitable linker sequences (1) will adopt a flexible extended conformation, (2) will not exhibit a propensity for developing an ordered secondary structure which could interact with the functional domains of fusion proteins, and (3) will have minimal hydrophobic or charged character which could promote interaction with the functional protein domains. Typical surface amino acids in flexible protein regions include Gly, Asn and Ser. Virtually any permutation of amino acid sequences containing Gly, Asn and Ser would be expected to satisfy the above criteria for a linker sequence. Other near neutral amino acids, such as Thr and Ala, may also be used in the linker sequence. The length of the linker sequence may vary without significantly affecting the biological activity of the fusion protein. Linker sequences are unnecessary where the proteins being fused have non-essential N- or C-terminal amino acid regions which can be used to separate the functional domains and prevent steric interference.

CD40-L polypeptides may exist as soluble polypeptides comprising the extracellular domain of CD40-L as shown in Figure 1 (SEQ ID NO:1) and Figure 2 (SEQ ID NO:11) or as membrane-bound polypeptides comprising the extracellular domain, a transmembrane region and a short intracellular domain, as shown in Figure 1 (SEQ ID NO:1) and Figure 2 (SEQ ID NO:11) for the murine and human sequences, respectively. Moreover, the present invention comprises oligomers of CD40-L extracellular domains or fragments thereof, linked by disulfide interactions, or expressed as fusion polymers with or without spacer amino acid linking

groups. For example, a dimer CD40-L molecule can be linked by an IgG Fc region linking group.

Without being bound by theory, membrane-bound CD40-L and oligomeric CD40-L can achieve activity stimulating Ig formation and proliferation of B cells previously only achieved by cross-linked anti-CD40 antibody in the presence of IL-4. It further appears likely that monomeric soluble CD40-L, comprising only the extracellular domain of CD40-L and capable of binding to CD40 receptor, will serve to antagonize the activity of membrane-bound and oligomeric CD40-L and/or cross-linked anti-CD40 antibodies. It further appears likely that the interaction of membrane-bound CD40-L with CD40 is the principal molecular interaction responsible for T cell contact dependent induction of B cell growth and differentiation to both antigen specific antibody production and polyclonal Ig secretion. In this regard, a mammalian cell transfected with a cDNA encoding full length CD40-L (i.e., being membrane-bound and having an intracellular domain, a transmembrane region and an extracellular domain or a fragment thereof) can mimic T cells in their ability to induce B cell growth, differentiation and stimulation of antigen-specific antibody production. It appears that activities of oligomeric soluble CD40-L, preferably an oligomer of extracellular regions, can mimic the biological activities of membrane-bound CD40-L. Moreover, soluble monomeric CD40-L (comprising the extracellular domain or a fragment thereof) can bind to CD40 receptor to prevent T cell interaction with B cells and therefor have activity similar to CD40 (receptor) extracellular domain which itself may be in monomeric or in oligomeric form. Alternatively, CD40-L can be oligomeric to act as a soluble factor capable of inducing B cell growth, differentiation and stimulation of antigen-specific antibody production. Accordingly, it appears that membrane-bound CD40-L and oligomeric CD40-L act as CD40 agonists, while soluble (monomeric) CD40-L and soluble CD40 act as CD40 antagonists by blocking CD40 receptor sites without significantly transducing signal or by preventing CD40-L binding to CD40 sites on B cells and other target cells.

Both CD40 agonists and CD40 antagonists will have useful therapeutic activity. For example, CD40 agonists (i.e., membrane-bound CD40-L and oligomeric CD40-L) are useful as vaccine adjuvants and for stimulating mAb production from hybridoma cells. CD40 antagonists (i.e., CD40 receptor, CD40/Fc and possibly soluble, monomeric CD40-L) are useful for treating autoimmune diseases characterized by presence of high levels of antigen-antibody complexes, such as allergy, lupus, rheumatoid arthritis, insulin dependent diabetes mellitus (IDDM), graft versus host disease (GVHD) and others.

IgE secretion from human B cells can be induced by IL-4 in the presence of T cells (Vercelli et al., *J. Exp. Med.* 169:1295, 1989). Further, IgE production can be induced from T cell depleted PBM (peripheral blood mononuclear cells) by addition of an anti-CD40 mAb (Jabara et al., *J. Exp. Med.* 172:1861, 1990 and Zhang et al., *J. Immunol.* 146:1836, 1991). The present invention further includes a method for inhibiting IgE production from activated B cells, activated by IL-4 in the presence of T cells or by CD40-L (preferably, membrane-bound

CD40-L), comprising administering an effective amount of a CD40/Fc fusion protein, as described herein, or a soluble CD40 encoded by the cDNA sequence described in SEQ ID NO. 3. Similarly, CD40 receptors and possibly soluble CD40-L (monomer only) can also block secretion of other antibody isotypes.

5 The present invention further includes CD40-L polypeptides with or without associated native-pattern glycosylation. CD40-L expressed in yeast or mammalian expression systems (e.g., COS-7 cells) may be similar to or significantly different from a native CD40-L polypeptide in molecular weight and glycosylation pattern, depending upon the choice of expression system. Expression of CD40-L polypeptides in bacterial expression systems, such as *E. coli*, provides non-glycosylated molecules.

10 DNA constructs that encode various additions or substitutions of amino acid residues or sequences, or deletions of terminal or internal residues or sequences not needed for biological activity or binding can be prepared. For example, the extracellular CD40-L N-glycosylation site can be modified to preclude glycosylation while allowing expression of a homogeneous, reduced carbohydrate analog using yeast expression systems. N-glycosylation sites in eukaryotic polypeptides are characterized by an amino acid triplet Asn-X-Y, wherein X is any amino acid except Pro and Y is Ser or Thr. Appropriate modifications to the nucleotide sequence encoding this triplet will result in substitutions, additions or deletions that prevent attachment of carbohydrate residues at the Asn side chain. In another example, sequences encoding Cys residues can be altered to cause the Cys residues to be deleted or replaced with other amino acids, preventing formation of incorrect intramolecular disulfide bridges upon renaturation. Human CD40-L comprises five Cys residues in its extracellular domain. Thus, at least one of the five Cys residues can be replaced with another amino acid or deleted without effecting protein tertiary structure or disulfide bond formation.

15 Other approaches to mutagenesis involve modification of sequences encoding dibasic amino acid residues to enhance expression in yeast systems in which KEX2 protease activity is present. Sub-units of a CD40-L polypeptide may be constructed by deleting sequences encoding terminal or internal residues or sequences. Moreover, other analyses may be performed to assist the skilled artisan in selecting sites for mutagenesis. For example, PCT/US92/03743 (the disclosure of which is hereby incorporated by reference) discusses methods of selecting ligand agonists and antagonists.

20 CD40-L polypeptides are encoded by multi-exon genes. The present invention further includes alternative mRNA constructs which can be attributed to different mRNA splicing events following transcription and which share regions of identity or similarity with the cDNAs disclosed herein.

25 Antisense or sense oligonucleotides comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target CD40-L mRNA (sense) or CD40-L DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of SEQ ID NO:1 or SEQ ID NO:11, or a DNA or RNA complement of

SEQ ID NO:1 or SEQ ID NO:11. Such a fragment comprises at least about 14 nucleotides. Preferably, such a fragment comprises from about 14 to about 30 nucleotides. The ability to create an antisense or a sense oligonucleotide, based upon a cDNA sequence for CD40-L is described in, for example, Stein and Cohen, *Cancer Res.* 48:2659, 1988 and van der Krol et al., *BioTechniques* 6:958, 1988.

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block translation (RNA) or transcription (DNA) by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. Suitable polymerase promoters include promoters for any RNA polymerase, or promoters for any DNA polymerase. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences. Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10448, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence. Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO₄-mediated DNA transfection, electroporation, or other gene transfer vectors such as Epstein-Barr virus. Antisense or sense oligonucleotides are preferably introduced into a cell containing the target nucleic acid sequence by insertion of the antisense or sense oligonucleotide into a suitable retroviral vector, then contacting the cell with the retrovirus vector containing the inserted sequence, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see PCT Application US 90/02656). Alternatively, other promoter sequences may be used to express the oligonucleotide.

Sense or antisense oligonucleotides may also be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

5 The sequence of murine CD40-L cDNA was obtained by direct expression techniques. The sequence of human CD40-L was obtained by cross-species hybridization techniques using the murine CD40-L cDNA as a probe.

10 We cloned murine CD40-L by first obtaining a clone of the extracellular region of human CD40 (the receptor) by polymerase chain reaction (PCR) techniques using primers based upon a sequence published in Stamenkovic et al. (SEQ ID NO:4). An upstream oligonucleotide primer 5'-CCGTCGACCACCATGGTTCGTCTGCC -3' (SEQ ID NO:5) introduces a *Sal* I site upstream from an initiator methionine of CD40 and a downstream oligonucleotide primer 5'-CCGTCGACGTCTAGAGCCGATCCTGGGG-3' (SEQ ID NO:6) inserts a termination codon after amino acid 192 of CD40, followed by *Xba* I and *Sal* I sites. 15 The amplified cDNA was digested with *Sal* I and cloned into pDC406 (McMahan et al., *EMBO J.* 10:2821, 1991) to construct pDC406/s CD40.

20 A second CD40 receptor fragment (SEQ ID NO:4) was obtained by PCR techniques for fusion to the Fc domain of human IgG1 (SEQ ID NO:3). Briefly, The upstream oligonucleotide primer (SEQ ID NO:5) and fusion template (SEQ ID NO:4) were the same as before. The downstream oligonucleotide primer was 5'-ACAAGATCTGGGCTCTACGTATCTCAGCCGATCCTGGGGAC-3' (SEQ ID NO:7) that inserts amino acids Tyr Val Glu Pro Arg (SEQ ID NO:8) after amino acid 193 of CD40. Glu and Pro are the first two amino acids of a hinge region of human IgG1, and are followed by a *Bgl* II restriction site. The *Bgl* II restriction site was used to fuse the extracellular domain of 25 CD40 to the remainder of human IgG1 Fc region.

30 Other fusion proteins comprising ligand binding domains from other receptors can be made by obtaining a DNA sequence for the ligand binding domain of a receptor and fusing this sequence to a DNA sequence encoding an Fc region of an antibody molecule that binds to protein A or protein G, or another polypeptide that is capable of affinity purification, for example, avidin or streptavidin. The resultant gene construct can be introduced into mammalian cells to transiently express a fusion protein. Receptor/Fc fusion proteins can be purified by protein A or protein G affinity purification. Receptor/avidin fusion proteins can be purified by biotin affinity chromatography. The fusion protein can later be removed from the column by eluting with a high salt solution or another appropriate buffer.

35 We obtained a cDNA encoding human IgG1 Fc region by PCR amplification using cDNA from human cells as a template and an upstream oligonucleotide primer 5'-TATTAATCATTCAGTAGGGCCCAGATCTTGTGACAAACTCAC-3' (SEQ ID NO:9) and a downstream oligonucleotide primer 5'-GCCAGCTTAAGTTCATTTACCCGGAGACAGGGAGA-3' (SEQ ID NO:10). The

PCR amplified cDNA introduced a *Bgl* II site near the beginning of the hinge region, which was used to ligate CD40 extracellular domain to construct a s CD40/Fc fusion cDNA, which was ligated into pDC406 to construct pDC406/CD40/Fc. Other suitable Fc regions are defined as any region that can bind with high affinity to protein A or protein G, and includes the Fc region of human IgG1 or murine IgG1. One example is the human IgG1 Fc region shown in SEQ ID NO:3 or the cDNA obtained by PCR from oligonucleotide primers from SEQ ID NO:9 and SEQ ID NO:10 with human cDNA as a template.

Receptor/Fc fusion molecules preferably are synthesized in recombinant mammalian cell culture because they are generally too large and complex to be synthesized by prokaryotic expression methods. Examples of suitable mammalian cells for expressing a receptor/Fc fusion protein include CV-1 cells (ATCC CCL 70) and COS-7 cells (ATCC CRL 1651), both derived from monkey kidney.

The DNA construct pDC406/CD40/Fc was transfected into the monkey kidney cell line CV-1/EBNA (ATCC CRL 10478). The pDC406 plasmid includes regulatory sequences derived from SV40, human immunodeficiency virus (HIV), and Epstein-Barr virus (EBV). The CV-1/EBNA cell line was derived by transfection of the CV-1 cell line with a gene encoding Epstein-Barr virus nuclear antigen-1 (EBNA-1) and constitutively express EBNA-1 driven from human CMV immediate-early enhancer/promoter. An EBNA-1 gene allows for episomal replication of expression vectors, such as pDC406, that contain the EBV origin of replication.

Transfectants expressing CD40/Fc fusion protein are initially identified using dot blots or Western blots. The supernatants are then subjected to dot blot or gel electrophoresis followed by transfer of the electrophoresed proteins for binding to G28-5 mAb (an antibody that binds to human CD40 receptor). The blotted proteins were then incubated with radiolabeled with ¹²⁵I-protein A, washed to remove unbound label, and examined for expression of Fc. Monoclonal antibody G28-5 was produced according to Clark et al., *supra*.

Once cells expressing the fusion construct were identified, large scale cultures of transfected cells were grown to accumulate supernatant from cells expressing CD40/Fc. CD40/Fc fusion protein in supernatant fluid was purified by affinity purification. Briefly, one liter of culture supernatant containing CD40/Fc fusion protein was purified by filtering mammalian cell supernatants (e.g., in a 0.45μ filter) and applying filtrate to a protein A/G antibody affinity column (Schleicher and Schuell, Keene, NH) at 4°C at a flow rate of 80 ml/hr for a 1.5 cm x 12.0 cm column. The column was washed with 0.5 M NaCl in PBS until free protein could not be detected in wash buffer. Finally, the column was washed with PBS. Bound fusion protein was eluted from the column with 25 mM citrate buffer, pH 2.8, and brought to pH 7 with 500 mM Hepes buffer, pH 9.1. Silver-stained SDS gels of the eluted CD40/Fc fusion protein showed it to be > 98% pure.

Soluble CD40 (sCD40) and CD40/Fc fusion proteins were made as described herein. The supernatants were purified through a G28-5 (anti-CD40 mAb) affinity column to affinity

purify sCD40 expressed by the transfected CV-1/EBNA cells. Protein-containing fractions were pooled and aliquots removed for G28-5 binding assays and analysis by SDS-PAGE (sodium dodecyl sulfate polyacrylamide gel electrophoresis) in the presence of 1 mM dithiothreitol as a reducing agent. A single band was seen of molecular weight 28,100 daltons. In the absence of a reducing agent, SDS-PAGE analysis of sCD40 revealed two bands, a major band of molecular weight 56,000 and a minor band of molecular weight 28,000. The banding pattern indicates that the majority of sCD40 exists as a disulfide-linked homodimer in solution. The 28,000 band is free monomer.

CD40 proteins were visualized by silver staining. Sample protein concentrations were determined using a micro-BCA assay (Pierce) with ultrapure bovine serum albumin as standard. Soluble CD40 purity and protein concentration were confirmed by amino acid analysis. Purified soluble CD40 was absorbed to PVDF paper and the paper subjected to automated Edman degradation on an Applied Biosystems model 477A protein sequencer according to manufacturers instructions for N-terminal protein sequencing. This procedure checked the protein sequence of sCD40.

Soluble CD40 and CD40/Fc fusion protein were able to modulate human B cell responses in the absence of anti-CD40 mAb (G28-5). Purified tonsillar B cells were cultured with anti-IgM and human IL-4 and either sCD40 or CD40/Fc fusion protein was added. Neither form of CD40 had an inhibitory effect on B cell proliferation (as measured by tritiated thymidine incorporation). IL-4 receptor, by contrast, inhibited IL-4-induced B cell proliferation in a concentration-dependent manner.

Soluble CD40 and CD40/Fc were tested for their ability to inhibit IL-4 induced IgE secretion in a 2-donor MLC (mixed lymphocyte culture) system. In three experiments, the level of IgE production was reduced as the concentration of CD40 was increased. Soluble CD40, added at a concentration of 10 µg/ml, was able to completely inhibit IgE secretion in this model of allergy. Further, CD40/Fc had similar effects as its soluble counterpart. However, addition of an IL-7 receptor-Fc fusion protein (made by similar procedures with a published IL-7 receptor sequence) did not affect secretion of IgE in this model.

Levels of CD23 were also measured in the same MLC in response to sCD40 or CD40/Fc fusion proteins. Soluble CD40 produced a small, but reproducible decrease in sCD23 level at day 6 compared to cultures stimulated with IL-4 alone, however a stronger inhibitory effect was pronounced at day 12 in the same cultures. Soluble CD23 induction by IL-4-stimulated T-depleted PBM (peripheral blood macrophages) E⁻ cells was similarly affected by addition of sCD40, causing a small decrease in sCD23 levels at day 6 and a more pronounced inhibition at day 12. In each culture system, the results with CD40/Fc fusion protein were substantially the same as with sCD40.

In an effort to isolate a cDNA for a CD40-L, purified CD40/Fc fusion protein was radioiodinated with ¹²⁵I using a commercially available solid phase agent (IODO-GEN, Pierce). In this procedure, 5 µg of IODO-GEN were plated at the bottom of a 10 x 75 mm

glass tube and incubated for twenty minutes at 4° C with 75 µl of 0.1 M sodium phosphate, pH 7.4 and 20 µl (2 mCi) Na¹²⁵I. The solution was then transferred to a second glass tube containing 5 µg of CD40/Fc in 45 µl PBS (phosphate buffered saline) and this reaction mixture was incubated for twenty minutes at 4° C. The reaction mixture was fractionated by gel
5 filtration on a 2 ml bed volume of Sephadex® G-25 (Sigma), and then equilibrated in RPMI 1640 medium containing 2.5% (v/v) bovine serum albumin (BSA), 0.2% (v/v) sodium azide and 20 mM Hepes, pH 7.4 binding medium. The final pool of ¹²⁵I CD40/Fc was diluted to a working stock solution of 1 x 10⁻⁷ M in binding medium and stored for up to one month at 4° C without detectable loss of receptor binding activity.

10 A cDNA library was prepared from a EL4 cell line sorted by FACS (fluorescence activated cell sorting) on the basis of binding of a biotinylated CD40/Fc fusion protein. Cells were sorted five times until there was a significant shift in fluorescence intensity based upon expression of a ligand for CD40 by the sorted EL-4 cells. The five-times sorted cells were called EL-40.5 cells and these cells were cultured for the purposes of creating a cDNA library
15 from EL-40.5 mRNA. Briefly, cDNA was synthesized, inserted into empty pDC406 vector and transformed into *E. coli*. Transformants were pooled, and the DNA from the pools was isolated and transfected into CV1-EBNA cells to create an expression cloning library. Transfected CV1-EBNA cells were cultured on slides for three days to permit transient expression of CD40-L. The slides containing the transfected cells were then incubated with
20 radioiodinated CD40/Fc, washed to remove unbound CD40/Fc, and fixed with gluteraldehyde. The fixed slides were dipped in liquid photographic emulsion and exposed in the dark. After developing the slides, they were individually examined with a microscope and cells expressing CD40-L were identified by the presence of autoradiographic silver grains against a light background.

25 The expression cloning library from EL-40.5 cells was screened and one pool, containing approximately 2000 individual clones, was identified as positive for binding ¹²⁵I labeled CD40/Fc fusion protein. This pool was broken down into smaller pools of approximately 200 colonies. The smaller pools were screened as described above. One of the smaller pools was positive for CD40-L.

30 A single clone was isolated and sequenced by standard techniques, to provide the cDNA sequence and deduced amino acid sequence of murine CD40-L as shown in Figure 1 and SEQ ID NO:1.

35 The human homolog CD40-L cDNA was found by cross species hybridization techniques. Briefly, a human peripheral blood lymphocyte (PBL) cDNA library was made from peripheral blood lymphocytes treated with OKT3 antibody (ATCC, Rockville MD) that binds to CD3 (10 ng/ml) and interleukin-2 (IL-2, 10 ng/ml) for six days. The PBL cells were washed and then stimulated for 4 hours with 10 ng/ml PMA (phorbol myristate acetate, Sigma St Louis) and 500 ng/ml ionomycin (Calbiochem). Messenger RNA was isolated from stimulated PBL cells, cDNA formed and cDNA was ligated into *Eco* R1 linkers. Ligated

cDNA was inserted into the *Eco* R1 site of λ gt10 phage cloning vehicle (Gigapak[®] Stratagene, San Diego, CA) according to manufacturer's instructions. Phage were amplified, plated at densities of approximately 20,000 phage per 15 cm plate. and phage lifts were performed, as described in Maniatis et al., *Molecular Biology: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY, 1982 , pages 316-328. A murine probe was constructed corresponding to the coding region of murine CD40-L from nucleotide 13 to nucleotide 793 of SEQ ID NO:1 and Figure 1. This probe was hybridized to the PBL library phage lifts under conditions of moderate to severe stringency. Briefly, hybridization conditions were 6 X SSC, 1 X Denhardt's solution, 2 mM EDTA, 0.5% Np40 (Nonidet P-40 detergent) at 63 °C overnight. This was followed by washing in 3 X SSC, 0.1% SDS for three hours at 55°C, followed by overnight exposure to X-Ray film. Positive plaques were identified at a frequency of approximately 1 per 1000 plaques. Positive plaques were purified twice and cDNA was prepared from amplified cultures.

One can utilize the murine or human CD40-L cDNA sequences disclosed herein to obtain cDNAs encoding other mammalian homologs of murine or human CD40-L by cross-species hybridization techniques. Briefly, an oligonucleotide probe is created from the nucleotide sequence of the extracellular region of murine CD40-L as described in Figure 1 (SEQ ID NO:1) or human CD40-L as described in Figure 2 (SEQ ID NO:11). This probe can be made by standard techniques, such as those described in Maniatis et al. *supra*. The murine or human probe is used to screen a mammalian cDNA library or genomic library under moderate stringency conditions. Examples of mammalian cDNA or genomic libraries include, for cDNA, a library made from the mammal's peripheral blood lymphocytes. Alternatively, various cDNA libraries or mRNAs isolated from various cell lines can be screened by Northern hybridization to determine a suitable source of mammalian CD40-L DNA or mRNA.

Recombinant expression vectors for expression of CD40-L by recombinant DNA techniques include a CD40-L DNA sequence comprising a synthetic or cDNA-derived DNA fragment encoding a CD40-L polypeptide, operably linked to a suitable transcriptional or translational regulatory nucleotide sequence, such as one derived from a mammalian, microbial, viral, or insect gene. Examples of regulatory sequences include sequences having a regulatory role in gene expression (e.g., a transcriptional promoter or enhancer), optionally an operator sequence to control transcription, a sequence encoding an mRNA ribosomal binding site, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are operably linked when the regulatory sequence functionally relates to the CD40-L DNA sequence. Thus, a promoter nucleotide sequence is operably linked to a CD40-L DNA sequence if the promoter nucleotide sequence controls the transcription of the CD40-L DNA sequence. Still further, a ribosome binding site may be operably linked to a sequence for a CD40-L polypeptide if the ribosome binding site is positioned within the vector to encourage translation. In addition, sequences encoding signal peptides can be incorporated into expression vectors. For example, a DNA sequence for a

signal peptide (secretory leader) may be operably linked to a CD40-L DNA sequence. The signal peptide is expressed as a precursor amino acid sequence which enables improved extracellular secretion of translated fusion polypeptide by a yeast host cell.

Suitable host cells for expression of CD40-L polypeptides include prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example, *E. coli* or *Bacilli*. Suitable prokaryotic host cells for transformation include, for example, *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various other species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. Higher eukaryotic cells include established cell lines of mammalian origin. Cell-free translation systems could also be employed to produce CD40-L polypeptides using RNAs derived from DNA constructs disclosed herein. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described, for example, in Pouwels et al. *Cloning Vectors: A Laboratory Manual*, Elsevier, New York, (1985).

In a prokaryotic host cell, such as *E. coli*, a CD40-L polypeptide or analog may include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal Met may be cleaved from the expressed recombinant CD40-L polypeptide. Prokaryotic host cells may be used for expression of CD40-L polypeptides that do not require extensive proteolytic or disulfide processing.

The expression vectors carrying the recombinant CD40-L DNA sequence are transfected or transformed into a substantially homogeneous culture of a suitable host microorganism or mammalian cell line. Transformed host cells are cells which have been transformed or transfected with nucleotide sequences encoding CD40-L polypeptides and express CD40-L polypeptides. Expressed CD40-L polypeptides will be located within the host cell and/or secreted into culture supernatant fluid, depending upon the nature of the host cell and the gene construct inserted into the host cell.

Expression vectors transfected into prokaryotic host cells generally comprise one or more phenotypic selectable markers. A phenotypic selectable marker is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement, and an origin of replication recognized by the host to ensure amplification within the host. Other useful expression vectors for prokaryotic host cells include a selectable marker of bacterial origin derived from commercially available plasmids. This selectable marker can comprise genetic elements of the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. The pBR322 "backbone" sections are combined with an appropriate promoter and a CD40-L DNA sequence. Other commercially vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA).

Promoter sequences are commonly used for recombinant prokaryotic host cell expression vectors. Common promoter sequences include β -lactamase (penicillinase), lactose

promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EP-A-36776) and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful prokaryotic host cell expression system employs a phage λ P_L promoter and a cI857ts thermolabile repressor sequence. Plasmid vectors available from the American Type Culture Collection which incorporate derivatives of the λ P_L promoter include plasmid pHUB2 (resident in *E. coli* strain JMB9 (ATCC 37092)) and pPLc28 (resident in *E. coli* RR1 (ATCC 53082)).

CD40-L may be expressed in yeast host cells, preferably from the *Saccharomyces* genus (e.g., *S. cerevisiae*). Other genera of yeast, such as *Pichia* or *Kluyveromyces*, may also be employed. Yeast vectors will often contain an origin of replication sequence from a 2 μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, and sequences for transcription termination. Preferably, yeast vectors include an origin of replication sequence and selectable marker. Suitable promoter sequences for yeast vectors include promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Hitzeman, EPA-73,657.

Yeast vectors can be assembled, for example, using DNA sequences from pBR322 for selection and replication in *E. coli* (Amp^r gene and origin of replication). Other yeast DNA sequences that can be included in a yeast expression construct include a glucose-repressible ADH2 promoter and α -factor secretion leader. The ADH2 promoter has been described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). The yeast α -factor leader sequence directs secretion of heterologous polypeptides. The α -factor leader sequence is often inserted between the promoter sequence and the structural gene sequence. See, e.g., Kurjan et al., *Cell* 30:933, 1982 and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. Other leader sequences suitable for facilitating secretion of recombinant polypeptides from yeast hosts are known to those of skill in the art. A leader sequence may be modified near its 3' end to contain one or more restriction sites. This will facilitate fusion of the leader sequence to the structural gene.

Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978. The Hinnen et al. protocol selects for Trp⁺ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μ g/ml adenine and 20 μ g/ml uracil.

Yeast host cells transformed by vectors containing ADH2 promoter sequence may be grown for inducing expression in a "rich" medium. An example of a rich medium is one consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 µg/ml adenine and 80 µg/ml uracil. Derepression of the ADH2 promoter occurs when glucose is exhausted from the medium.

Mammalian or insect host cell culture systems could also be employed to express recombinant CD40-L polypeptides. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., *Cell* 23:175, 1981), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, and BHK (ATCC CRL 10) cell lines. Suitable mammalian expression vectors include nontranscribed elements such as an origin of replication, a promoter sequence, an enhancer linked to the structural gene, other 5' or 3' flanking nontranscribed sequences, such as ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences.

Transcriptional and translational control sequences for mammalian host cell expression vectors may be excised from viral genomes. For example, commonly used mammalian cell promoter sequences and enhancer sequences are derived from Polyoma virus, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites may be used to provide the other genetic elements required for expression of a structural gene sequence in a mammalian host cell. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome as a fragment which may also contain a viral origin of replication (Fiers et al., *Nature* 273:113, 1978). Smaller or larger SV40 fragments may also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* I site located in the SV40 viral origin of replication site is included.

Exemplary mammalian expression vectors can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983). A useful high expression vector, PMLSV N1/N4, described by Cosman et al., *Nature* 312:768, 1984 has been deposited as ATCC 39890.

Additional useful mammalian expression vectors are described in EP-A-0367566, and in U.S. Patent Application Serial No. 07/701,415, filed May 16, 1991, incorporated by reference herein. For expression of a type II protein extracellular region, such as CD40-L, a heterologous signal sequence should be added, such as the signal sequence for interleukin-7 (IL-7) described in United States Patent 4,965,195, or the signal sequence for interleukin-2 receptor described in United States Patent Application 06/626,667 filed on July 2, 1984.

Human or murine CD40-L can be made in membrane-bound form when an intracellular and transmembrane regions are included or in soluble form with only the extracellular domain. We expressed full length murine CD40-L in mammalian cells to yield cells expressing membrane-bound murine CD40-L. CV1 cells were transfected with a cDNA shown in Figure

1 (SEQ ID NO:1) in HAVEO vector or CV1 cells were transfected with HAVEO empty vector using techniques described in Example 6 herein. This yielded transfected CV1 cells expressing membrane-bound murine CD40-L. These cells were used as a source of membrane-bound murine CD40-L for the series of experiments reported in Examples 10 -13 reported below.

Purification of Recombinant CD40-L Polypeptides

CD40-L polypeptides may be prepared by culturing transformed host cells under culture conditions necessary to express CD40-L polypeptides. The resulting expressed polypeptides may then be purified from culture media or cell extracts. A CD40-L polypeptide, if desired, may be concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a purification matrix such as a gel filtration medium.

Alternatively, an anion exchange resin can be employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Sulfopropyl groups are preferred.

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, (e.g., silica gel having pendant methyl or other aliphatic groups) can be employed to further purify CD40-L. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous recombinant protein.

It is also possible to utilize an affinity column comprising CD40 ligand binding domain to affinity-purify expressed CD40-L polypeptides. CD40-L polypeptides can be removed from an affinity column in a high salt elution buffer and then dialyzed into a lower salt buffer for use.

Recombinant protein produced in bacterial culture is usually isolated by initial disruption of the host cells, centrifugation, extraction from cell pellets if an insoluble polypeptide, or from the supernatant fluid if a soluble polypeptide, followed by one or more concentration, salting-out, ion exchange, affinity purification or size exclusion chromatography steps. Finally, RP-HPLC can be employed for final purification steps. Microbial cells can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Transformed yeast host cells are preferably employed to express CD40-L as a secreted polypeptide. This simplifies purification. Secreted recombinant polypeptide from a yeast host cell fermentation can be purified by methods analogous to those disclosed by Urdal et al. (*J. Chromatog.* 296:171, 1984). Urdal et al. describe two sequential, reversed-phase HPLC steps for purification of recombinant human IL-2 on a preparative HPLC column.

Administration of CD40-L Compositions

The present invention provides therapeutic compositions comprising an effective amount of CD40-L in a suitable diluent or carrier and methods of treating mammals using the compositions. For therapeutic use, purified CD40-L or a biologically active analog thereof is administered to a patient, preferably a human, for treatment in a manner appropriate to the indication. Thus, for example, CD40-L pharmaceutical compositions (for example, in the form of a soluble extracellular domain, or a fragment thereof) which is administered to achieve a desired therapeutic effect can be given by bolus injection, continuous infusion, sustained release from implants, or other suitable technique. Typically, a CD40-L therapeutic agent will be administered in the form of a pharmaceutical composition comprising purified CD40-L polypeptide in conjunction with physiologically acceptable carriers, excipients or diluents. Such carriers will be nontoxic to patients at the dosages and concentrations employed. Ordinarily, the preparation of such compositions entails combining a CD40-L polypeptide with buffers, antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, proteins, amino acids, carbohydrates including glucose, sucrose or dextrans, chelating agents such as EDTA, glutathione and other stabilizers and excipients. Neutral buffered saline or saline mixed with conspecific serum albumin are exemplary appropriate diluents. CD40-L sense or antisense oligonucleotides may be administered *in vivo* by administering an effective amount of a vector containing a nucleic acid sequence that encodes and effective antisense or sense oligonucleotide. Additionally, CD40-L sense or antisense oligonucleotides may be administered *ex vivo* by removing cells containing CD40-L DNA or mRNA from an individual, incorporating an antisense or sense oligonucleotide into the cells using gene transfer techniques, and re-infusing the cells into the individual.

The following examples are intended to illustrate particular embodiments and not limit the scope of the invention.

EXAMPLE 1

This example describes construction of a CD40/Fc DNA construct to express a soluble CD40/Fc fusion protein for use in detecting cDNA clones encoding a CD40 ligand. The cDNA sequence of the extracellular region or ligand binding domain of complete CD40 human receptor sequence was obtained using polymerase chain reaction (PCR) techniques, and is based upon the sequence published in Stamenkovic et al., *supra*. A CD40 plasmid (CDM8) was used as a template for PCR amplification. CDM8 is described in Stamenkovic et al. and was obtained from the authors. A PCR technique (Sarki et al., *Science* 239:487, 1988) was employed using 5' (upstream) and 3' (downstream) oligonucleotide primers to amplify the DNA sequences encoding CD40 extracellular ligand binding domain. Upstream oligonucleotide primer 5'-CCGTCGACCACCATGGTTCGTCTGCC -3' (SEQ ID NO:5) introduces a *Sal* I site upstream from an initiator methionine of CD40 and a downstream oligonucleotide primer 5'-

ACAAGATCTGGGCTCTACGTATCTCAGCCGATCCTGGGGAC-3' (SEQ ID NO:7) that inserts amino acids Tyr Val Glu Pro Arg (SEQ ID NO:8) after amino acid 193 of CD40. Glu and Pro are the first two amino acids of a hinge region of human IgG1, and are followed by a *Bgl* II restriction site that was used to fuse the extracellular domain of CD40 to the remained of human IgG1 Fc region.

The DNA construct pDC406/CD40/Fc was transfected into the monkey kidney cell line CV-1/EBNA (ATCC CRL 10478). The pDC406 plasmid includes regulatory sequences derived from SV40, human immunodeficiency virus (HIV), and Epstein-Barr virus (EBV). The CV-1/EBNA cell line was derived by transfection of the CV-1 cell line with a gene encoding Epstein-Barr virus nuclear antigen-1 (EBNA-1) that constitutively expresses EBNA-1 driven from the human CMV intermediate-early enhancer/promoter. The EBNA-1 gene allows for episomal replication of expression vectors, such as pDC406, that contain the EBV origin of replication.

Once cells expressing the fusion construct were identified, large scale cultures of transfected cells were grown to accumulate supernatant from cells expressing CD40/Fc. The CD40/Fc fusion protein in supernatant fluid was purified by affinity purification. Briefly, one liter of culture supernatant containing the CD40/Fc fusion protein was purified by filtering mammalian cell supernatants (e.g., in a 0.45 μ filter) and applying filtrate to a protein A/G antibody affinity column (Schleicher and Schuell, Keene, NH) at 4°C at a flow rate of 80 ml/hr for a 1.5 cm x 12.0 cm column. The column was washed with 0.5 M NaCl in PBS (phosphate buffered saline) until free protein could not be detected in wash buffer. Finally, the column was washed with PBS. Bound fusion protein was eluted from the column with 25 mM citrate buffer, pH 2.8, and brought to pH 7 with 500 mM Hepes buffer, pH 9.1. Silver-stained SDS gels of the eluted CD40/Fc fusion protein showed it to be > 98% pure.

Purified CD40/Fc fusion protein was iodinated with ¹²⁵I using a commercially available solid phase agent (IODO-GEN, Pierce). In this procedure, 5 μ g of IODO-GEN were plated at the bottom of a 10 x 75 mm glass tube and incubated for twenty minutes at 4° C with 75 μ l of 0.1 M sodium phosphate, pH 7.4 and 20 μ l (2 mCi) Na¹²⁵I. The solution was then transferred to a second glass tube containing 5 μ g of CD40/Fc in 45 μ l PBS and this reaction mixture was incubated for twenty minutes at 4° C. The reaction mixture was fractionated by gel filtration on a 2 ml bed volume of Sephadex® G-25 (Sigma), and then equilibrated in RPMI 1640 medium containing 2.5% (v/v) bovine serum albumin (BSA), 0.2% (v/v) sodium azide and 20 mM Hepes, pH 7.4 binding medium. The final pool of ¹²⁵I CD40/Fc was diluted to a working stock solution of 1 x 10⁻⁷ M in binding medium and stored for up to one month at 4° C without detectable loss of receptor binding activity.

Approximately 50% - 60% label incorporation was observed. Radioiodination yielded specific activities in the range of 1 x 10¹⁵ to 5 x 10¹⁵ cpm/nmole (0.42 - 2.0 atoms of radioactive iodine per molecule of protein). SDS polyacrylamide gel electrophoresis (SDS-PAGE) revealed a single labeled polypeptide consistent with expected values. The labeled

fusion protein was greater than 98% trichloroacetic acid (TCA) precipitable, indicating that the ¹²⁵I was covalently bound to the protein.

EXAMPLE 2

This example describes selection of a cell line putatively expressing CD40-L. Several cell lines were screened using the radioiodinated CD40/Fc fusion protein described in Example 1. Briefly, quantitative binding studies were performed according to standard methodology, and Scatchard plots were derived for the various cell lines. A clonal cell line (EL4, ATCC Catalog TIP 39) a murine thymoma cell line was identified and sorted. Prior to sorting, EL-4 cells were found to express approximately 450 molecules of CD40-L per cell. The seventh sort cells were called EL-40.7 and were grown and found to express approximately 10,000 molecules of CD40-L per cell. Lastly, the ninth sort cells were called EL-40.9 and were grown and found to express approximately 15,000 molecules of CD40-L per cell.

EXAMPLE 3

This example describes preparation of a cDNA library for expression cloning of murine CD40-L. The library was prepared from a fifth sorted clone of a mouse thymoma cell line EL-4 (ATCC TIB 39), called EL-40.5. EL-40.5 cells were EL4 cells sorted five times with biotinylated CD40/Fc fusion protein in a FACS (fluorescence activated cell sorter). A cDNA library was made from RNA obtained from EL-40.5 cells essentially as described in US Patent 4,968,607, the disclosure of which is incorporated by reference herein. Briefly, a cDNA library was constructed by reverse transcription of poly (A)⁺ mRNA isolated from the total RNA extracted from the EL-40.5 cell line. The library construction technique was substantially similar to that described by Ausubel et al., eds., *Current Protocols In Molecular Biology*, Vol. 1, (1987). Poly (A)⁺ mRNA was isolated by oligo dT cellulose chromatography and double-stranded cDNA was made substantially as described by Gubler et al., *Gene* 25:263, 1983. Poly(A)⁺ mRNA fragments were converted to RNA-cDNA hybrids by reverse transcriptase using random hexanucleotides as primers. The RNA-cDNA hybrids were then converted into double-stranded cDNA fragments using RNAase H in combination with DNA polymerase I. The resulting double-stranded cDNA was blunt-ended with T4 DNA polymerase.

Sal I adaptors

5' - TCG ACT GGA ACG AGA CGA CCT GCT -3'
GA CCT TGC TCT GCT GGA CGA - 5'

were ligated to 5' ends of resulting blunt-ended cDNA, as described in Haymerle et al., *Nucleic Acids Res.* 14:8615, 1986. Non-ligated adaptors were removed by gel filtration chromatography at 68°C. This left 24 nucleotide non-self-complementary overhangs on cDNA. The same procedure was used to convert 5' *Sal I* ends of the mammalian expression vector pDC406 to 24 nucleotide overhangs complementary to those added to cDNA. Optimal proportions of adapted vector and cDNA were ligated in the presence of T4 polynucleotide

kinase. Dialyzed ligation mixtures were electroporated into *E. coli* strain DH5 α and transformants selected on ampicillin plates.

Plasmid DNA was isolated from pools consisting of approximately 2,000 clones of transformed *E. coli* per pool. The isolated DNA was transfected into a sub-confluent layer of CV1-EBNA cells using DEAE-dextran followed by chloroquine treatment substantially according to the procedures described in Luthman et al., *Nucl. Acids Res.* 11:1295, 1983 and McCutchan et al., *J. Natl. Cancer Inst.* 41:351, 1986.

CV1-EBNA cells were maintained in complete medium (Dulbecco's modified Eagles' media containing 10% (v/v fetal calf serum, 50 U/ml penicillin, 50 U/ml streptomycin, and 2 mM L-glutamine) and were plated to a density of approximately 2×10^5 cells/well in single-well chambered slides (Lab-Tek). The slides were pre-treated with 1 ml human fibronectin (10 μ g/ml PBS) for 30 minutes followed by a single washing with PBS. Media was removed from adherent cells growing in a layer and replaced with 1.5 ml complete medium containing 66.6 μ M chloroquine sulfate. About 0.2 ml of a DNA solution (2 μ g DNA, 0.5 mg/ml DEAE-dextran in complete medium containing chloroquine) was added to the cells and the mixture was incubated at 37°C for about five hours. Following incubation, media was removed and the cells were shocked by addition of complete medium containing 10% DMSO (dimethylsulfoxide) for 2.5 - 20 minutes. Shocking was followed by replacement of the solution with fresh complete medium. The cells were grown in culture for two to three days to permit transient expression of the inserted DNA sequences. These conditions led to a 30% to 80% transfection frequency in surviving CV1-EBNA cells.

EXAMPLE 4

This example describes screening of the expression cloning library made in Example 3 with a labeled CD40/Fc fusion protein made in Example 1. After 48 - 72 hours, transfected monolayers of CV1-EBNA cells made in Example 3 were assayed by slide autoradiography for expression of CD40-L using radioiodinated CD40/Fc fusion protein as prepared in Example 1. Transfected CV1-EBNA cells were washed once with binding medium (RPMI 1640 containing 25 mg/ml bovine serum albumin (BSA), 2 mg/ml sodium azide, 20 mM Hepes pH 7.2, and 50 mg/ml nonfat dry milk) and incubated for 2 hours at 4°C in binding medium containing 1×10^{-9} M 125 I-CD40/Fc fusion protein. After incubation, cells in the chambered slides were washed three times with binding buffer, followed by two washes with PBS, (pH 7.3) to remove unbound radiolabeled fusion protein.

The cells were fixed by incubating in 10% glutaraldehyde in PBS (30 minutes at room temperature), washed twice in PBS and air-dried. The slides were dipped in Kodak GTNB-2 photographic emulsion (6x dilution in water) and exposed in the dark for two to four days at room temperature in a light-proof box. The slides were developed in Kodak D19 developer, rinsed in water and fixed in Agfa G433C fixer. The slides were individually examined under a

microscope at 25-40x magnification. Positive slides showing cells expressing CD40-L were identified by the presence of autoradiographic silver grains against a light background.

One pool containing approximately 2000 individual clones was identified as potentially positive for binding the CD40/Fc fusion protein. The pool was titrated and plated to provide plates containing approximately 200 colonies each. Each plate was scraped to provide pooled plasmid DNA for transfection into CV1-EBNA cells according to the same procedure described above. The smaller pools were screened by slide autoradiography as described previously. One of the smaller pools contained clones that were positive for CD40-L as indicated by the presence of an expressed gene product capable of binding to the CD40/Fc fusion protein.

The positive smaller pool was titrated and plated to obtain individual colonies. Approximately 400 individual colonies were picked and inoculated into culture medium in individual wells of 96-well plates. Cultures were mixed by pooling rows and columns and the mixed cultures were used to prepare DNA for a final round of transfection and screening. An intersection of a positive row and a positive column indicated a potential positive colony. Ten potential positive colonies (i.e., candidate clones) were identified. DNA was isolated from each candidate clone, retransfected and rescreened. Five candidate clones were positive by binding to CD40/Fc. All five positive candidate clones contained a cDNA insert of 1468 nucleotides, as determined by dideoxynucleotide sequencing. The cDNA coding region of the CD40-L clone corresponds to the sequence of Figure 1 and SEQ ID NO:1.

A cloning vector containing murine CD40-L sequence, designated pDC406-mCD40-L, was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on December 6, 1991, under accession number 68872. The nucleotide sequence and predicted amino acid sequence of this clone are illustrated in SEQ ID NO:1 and in Figure 1.

EXAMPLE 5

This example illustrates a cross-species hybridization technique which was used to isolate a human CD40-L homolog using a probe designed from the sequence of murine CD40-L. A murine CD40-L probe was produced by excising the coding region from murine CD40-L clone pDC406-CD40-L (nucleotide 13 through 793) and ³²P-labeling the fragment using random primers (Boehringer-Mannheim).

A human peripheral blood lymphocyte (PBL) cDNA library was constructed in a λ phage vector using λ gt10 arms and packaged *in vitro* using a commercially available kit (Gigapak[®] Stratagene, San Diego, CA) according to the manufacturer's instructions. The PBL cells were obtained from normal human volunteers and treated with 10 ng/ml of OKT3 (an anti-CD3 antibody), and 10 ng/ml of human IL-2 (Immunex, Seattle, WA) for six days. The PBL cells were washed and stimulated with 500 ng/ml ionomycin (Calbiochem) and 10 ng/ml PMA (Sigma) for four hours. Messenger RNA and cDNA were obtained from the stimulated PBL cells and packaged into λ gt10 phage vectors (Gigapak[®] Stratagene) according to manufacturer's instructions.

The murine probe was hybridized to phage cDNA in 6 X SSC (15 mM trisodium citrate, and 165 mM sodium chloride), 1 X Denhardt's solution, 2 mM EDTA, 0.5% Np40 at 63°C overnight. Hybridization was followed by extensive washing in 3 X SSC, 0.1% SDS at approximately 55°C for three hours. Specific bands were visualized by autoradiography.

A cloning vector containing human CD40-L sequence, designated hCD40-L, was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on December 6, 1991, under accession number 68873. The nucleotide sequence and predicted amino acid sequence of this clone are illustrated SEQ ID NO:11 and in Figure 2.

EXAMPLE 6

This example illustrates the expression of membrane-bound murine CD40-L in CV1-EBNA cells. Murine CD40-L cDNA in HAVEO vector or empty HAVEO vector were transfected into CV1 EBNA cells using standard techniques, such as those described in McMahan et al. et al. *EMBO J.* 10:2821, 1991 and in Example 3 herein. Briefly, CV1 EBNA cells were plated at a density of 2×10^6 cells per 10 cm dish in 10 ml of Dulbecco's Minimal Essential Medium supplemented with 10% fetal calf serum (Medium). The cells were allowed to adhere overnight at 37°C. The Medium was replaced with 1.5 ml of Medium containing 66.7 µM chloroquine and a DNA mixture containing 5 µg of cDNA encoding mCD40-L. Medium containing 175 µl, and 25 µl of DEAE dextran (4 mg/ml in PBS) was also added to the cells. The cells and cDNA were incubated at 37°C for 5 hours. The cDNA mixture was removed and the cells were shocked with 1 ml of fresh Medium containing 10% DMSO for 2.5 min. The Medium was replaced with fresh Medium and the cells were grown for at least 3 days.

EXAMPLE 7

This example illustrates the preparation of monoclonal antibodies to CD40-L. Preparations of purified murine CD40-L or human CD40-L are prepared by COS cell expression and CD40/Fc affinity purification as described herein. Purified CD40-L or transfected cells expressing membrane-bound CD40-L can generate monoclonal antibodies against CD40-L using conventional techniques, for example, those techniques described in U.S. Patent 4,411,993. Briefly, mice are immunized with human CD40-L as an immunogen emulsified in complete Freund's adjuvant or another suitable adjuvant such as incomplete Freund's adjuvant or Ribi adjuvant R700 (Ribi, Hamilton, MT) or another suitable adjuvant, and injected in amounts ranging from 10-100 µg subcutaneously or intraperitoneally. Rats (i.e. Lewis rats) are immunized with murine CD40-L as an immunogen in a similar manner. Ten days to three weeks later, the immunized animals are boosted with additional CD40-L emulsified in incomplete Freund's adjuvant. Mice are periodically boosted thereafter on a weekly, bi-weekly or every third week immunization schedule. Serum samples are

periodically taken by retro-orbital bleeding or tail-tip excision for testing by dot blot assay, ELISA (Enzyme-Linked Immunosorbent Assay), or FACS analysis, for CD40-L antibodies.

Following detection of an appropriate antibody titer, positive animals are provided one last intravenous injection of CD40-L in saline. Three to four days later, the animals are sacrificed, spleen cells harvested, and spleen cells are fused to a murine myeloma cell line (e.g., NS1 or Ag 8.653). Fusions generate hybridoma cells, which are plated in multiple microtiter plates in a selective medium containing HAT (hypoxanthine, aminopterin and thymidine) to inhibit proliferation of non-fused cells, myeloma-myeloma hybrids, and spleen cell-spleen cell hybrids.

The hybridoma cells are screened by ELISA for reactivity against purified CD40-L by adaptations of the techniques disclosed in Engvall et al., *Immunochem.* 8:871, 1971 and in U.S. Patent 4,703,004, or by or FACS as described herein. Positive hybridoma cells can be cloned in soft agar or another, similar medium, or by limiting dilution, to insure that a final cell population is derived from a single hybridoma cell. The cloned hybridoma cells are injected intraperitoneally into syngeneic mice (or rats) to produce ascites containing high concentrations of anti-CD40-L monoclonal antibodies. Alternatively, hybridoma cells can be grown *in vitro* in flasks or roller bottles by various techniques. Monoclonal antibodies produced in mouse ascites can be purified by ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can also be used, as can affinity chromatography based upon binding to CD40-L.

EXAMPLE 8

This example illustrates anti-allergy therapeutic effects of sCD40 and CD40/Fc fusion protein. Soluble CD40 and CD40/Fc were tested for their ability to inhibit IL-4 (5 ng/ml) induced IgE secretion in a two donor MLC system. The data from three experiments are presented in Table 1.

Table 1

IgE (ng/ml)

| Addition | Exp. 1 | Exp. 2 | Exp. 3 |
|----------------------------|--------|--------|--------|
| medium | <0.1 | <0.1 | <0.1 |
| IL-4 | 24 | 47 | 54 |
| IL-4 + sCD40 (0.1 µg/ml) | 19 | nd | 38 |
| IL-4 + sCD40 (0.3 µg/ml) | 14 | 29 | 24 |
| IL-4 + sCD40 (1 µg/ml) | 10 | 24 | 8 |
| IL-4 + sCD40 (3 µg/ml) | 7 | 19 | 2 |
| IL-4 + IL-7R/Fc (10 µg/ml) | 21 | nd | 58 |

IgE levels were measured after 12 days in culture by an ELISA procedure. Briefly, flat-bottomed 96-well microtiter plates (Corning) were coated with mouse mAb anti-human IgE (Zymed) at 1:500 dilution in PBS (phosphate buffered saline). After washing 3X, a blocking step was performed using 5% non-fat dried milk, followed by titration of human IgE standards or test supernatants. After washing 3X, biotinylated goat anti-human IgE (Kirkegaard and Perry) was added at a 1:500 dilution. This was followed by further washing and then addition of streptavidin-HRP (Zymed) at a 1:500 dilution. After further washing, the reaction was developed using TMB substrate (Kirkegaard and Perry) and absorbance measured at 520 nm. All washing steps were carried out in PBS plus 0.05% Tween. All incubation steps were performed at volumes of 100 µl/well for one hour at room temperature. The sensitivity of this assay is 100 pg/ml.

EXAMPLE 9

This example illustrates the effects of sCD40 and CD40/Fc fusion protein to inhibit soluble CD23 shedding from IL-4 (5 ng/ml) stimulated B cells. Soluble CD40 and CD40/Fc were tested for their ability to inhibit IL-4-induced sCD23 shedding in a two donor MLC system. The data from three experiments are presented in Table 2.

Table 2

| Addition | sCD23 (ng/ml) | | | | | |
|-----------------------------|---------------|--------|--------|--------|--------|--------|
| | Exp. 1 | | Exp. 2 | | Exp. 3 | |
| | day 6 | day 12 | day 6 | day 12 | day 6 | day 12 |
| E ⁻ + medium | 55 | <0.5 | 24 | 10 | 10 | 5 |
| + IL-4 | 115 | 55 | 96 | 62 | 44 | 27 |
| + IL-4 + sCD40 (1 µg/ml) | nd | nd | 88 | 36 | 38 | 9 |
| + IL-4 + sCD40 (3 µg/ml) | 97 | 4 | 82 | 31 | 40 | 4 |
| + IL-4 + sCD40 (10 µg/ml) | nd | nd | 72 | 28 | nd | nd |
| + IL-4 + IL-7R/Fc (3 µg/ml) | 111 | 48 | 103 | 67 | 40 | 22 |
| PBM + medium | 12 | <0.5 | 15 | 5 | 3 | 10 |
| + IL-4 | 39 | 255 | 47 | 22 | 48 | 26 |
| + IL-4 + sCD40 (1 µg/ml) | nd | nd | 44 | 18 | 46 | 18 |
| + IL-4 + sCD40 (3 µg/ml) | 24 | 6 | 37 | 11 | 45 | 12 |
| + IL-4 + sCD40 (10 µg/ml) | nd | nd | 28 | 5 | nd | nd |
| + IL-4 + IL-7R/Fc (3 µg/ml) | 35 | 26 | 43 | 20 | 50 | 23 |

Soluble CD23 levels were measured after 6 and 12 days in culture by a commercial sCD23 ELISA detection kit (Binding Site, San Diego, CA). The sensitivity limit was 500 pg/ml. Approximately 1×10^5 cells per well were cultured in triplicate in round-bottomed 96-well microtiter plates (Intermountain Scientific, Bountiful UT) for the indicated time in the

presence or absence of additives as indicated in Table 2. The results show anti-allergy effects of sCD40. Similar studies were run with CD40/Fc (data not shown) instead of sCD40, and similar results were obtained. Accordingly, these data in Examples 8 and 9 illustrate an anti-allergy property for CD40.

EXAMPLE 10

This example illustrates B cell proliferative activity of membrane-bound murine CD40-L for human B cells. Human peripheral blood mononuclear cells (PBMC) were isolated from peripheral blood from normal volunteers by density gradient centrifugation over Histopaque® (Sigma, St. Louis, MO). T cell-depleted preparations of cells (E^-) were obtained by removing T cells by rosetting with 2-aminoethylisothiuronium bromide-treated SRBC (sheep red blood cells) and further density gradient centrifugation over Histopaque®. B cell proliferation assays were conducted with E^- preparations in RPMI media with added 10% heat-inactivated fetal bovine serum (FBS) at 37°C in a 10% CO₂ atmosphere. Approximately 1×10^5 E^- cells per well were cultured in triplicate in flat-bottomed 96-well microtiter plates (Corning) for 7 days in the presence of transfected CV1 EBNA cells (described in Example 6). The CV1 EBNA cells were transfected with murine CD40-L cDNA or empty vector. The cells were pulsed with 1 μ Ci/well of tritiated thymidine (25 Ci/nmole Amersham, Arlington Heights, IL) for the final eight hours of culture. Cells were harvested onto glass fiber discs with an automated cell harvester and incorporated cpm were measured by liquid scintillation spectrometry.

Figure 4a shows a comparison of human B cell proliferation of CV1 EBNA cells transfected with empty vector (HAVEO) or with murine CD40-L cDNA in HAVEO vector. These data show that membrane-bound CD40-L stimulates human B cell proliferation in the absence of a co-mitogen. Figure 4b shows a similar experiment, except that 10 ng/ml of human IL-4 was added to the cultures. In this experiment, IL-4 slightly enhances the B cell mitogenic activity of membrane-bound murine CD40-L. Figure 5 is a repeat of the experiment shown in Figure 4b. However, when the experiment was repeated, there was no evidence of IL-4 co-mitogenic activity. There was repeated evidence of CD40-L mitogenic activity. Accordingly, membrane-bound CD40-L stimulates proliferation of human B cells.

EXAMPLE 11

This example illustrates the effect of membrane-bound murine CD40-L to stimulate IgE production and CD23 shedding from E^- cells isolated in Example 10. Approximately 1×10^5 cells/well were cultured in triplicate round bottomed 96-well Nunc microtiter plates (Intermountain Scientific, Bountiful UT) in Iscove's Modified Dulbecco's Medium (IMDM) plus 10% FCS in a humidified atmosphere of 10% CO₂. Medium was supplemented with 50 μ g/ml human transferrin (Sigma), 0.5% bovine serum albumin (Sigma) and 1 μ g/ml of each of oleic, linoleic and palmitic acids (Sigma). The E^- cells were cultured for 10 days in the presence of 5 ng/ml human IL-4. A titration of CV1 EBNA cells transfected with murine

CD40-L or empty vector were added. After ten days, culture supernatants were assayed for IgE by the ELISA procedure described in Example 8 or for CD23 shedding by the procedure described in Example 9.

Figure 6 shows a comparison of IgE production in the supernatants (in ng/ml) for cultures of E⁻ cells and CV1 EBNA cells transfected with empty vector (HAVEO) or with CD40-L. No differences were noted with up to 3000 CV1 EBNA cells, however significant IgE production resulted with the addition of 10000 or 30000 CD40-L transfected CV1 EBNA cells. As a comparison, when E⁻ cells were incubated with medium alone, 5 ng/ml IL-4 or 5 ng/ml IL-4 plus 500 ng/ml G28-5 antibody, IgE production was 4.7, 2.9 and >600 ng/ml, respectively. When CD23 shedding was measured in Figure 7, 10000 and 30000 CVI EBNA cells transfected with CD40-L showed increased CD23 shedding when compared to empty vector control CV1 EBNA cells. As a comparison, when E⁻ cells were incubated with medium alone, 5 ng/ml IL-4 or 5 ng/ml IL-4 plus 500 ng/ml G28-5 antibody, CD23 shedding was <0.1, 2.4 and 11.2 ng/ml, respectively. These data show that IgE production and CD23 shedding are both biological activities associated with membrane-bound CD40-L.

EXAMPLE 12

This example illustrates B cell proliferative activity, polyclonal immunoglobulin (Ig) production, antigen-specific antibody formation and various method for using membrane-bound and soluble CD40-L in clinical applications. We obtained murine splenic B cells according to procedures described in Grabstein et al. I *supra*, Maliszewski et al. I *supra* and Maliszewski et al. II *supra*. Briefly, the mixed culture of cells was purified by T cell depletion using T cell antiserum and complement, and adherent cell depletion by passage of Sephadex® G10 columns and by B cell positive selection by panning on petri dishes coated with goat anti-mouse IgM. Purified B cells were cultured in RPMI, fetal calf serum (5% for B cell proliferation assays and 20% for plaque forming cell assays or polyclonal antibody assays), 2-mercaptoethanol, antibiotics, amino acids and pyruvate. B cell proliferation was measured according to the assay described in Example 10 and in Grabstein et al. I *supra*, Maliszewski et al. I *supra* and Maliszewski et al. II *supra*. Antigen-specific antibody formation was measured by the procedure described in Grabstein et al., *J. Mol. Cell. Immunol.* 2:199, 1986 [Grabstein et al. II]. Briefly, antigen specific antibody formation used sheep red blood cells (SRBC) as antigen (0.03% v/v) in 2.0 ml cultures of 1 X 10⁶ murine B cells per culture. The B cell cultures were incubated for 5 days and plaque forming cells were determined by Jerne hemolytic plaque assay as described in Grabstein et al. II *supra*. Cell counts were determined in a coulter counter. Polyclonal Ig secretion was determined by isotype-specific ELISA assays in seven day cultures of 1 X 10⁶ B cells per 2.0 ml culture as described in Maliszewski et al. I *supra* and Maliszewski et al. II *supra*.

The results of B cell proliferation by CV1 EBNA cells transfected with CD40-L or empty vector or 7A1 cells (a T cell helper clone) are shown in Figures 8, 10 and 12. These data

show that the greatest B cell proliferation was caused by CD40-L. T cell helper cells 7A1 and 7C2 had a minimal effect on B cell proliferation.

The effects of various cells upon antigen specific antibody formation are shown in Figures 9 and 11. Figure 9 shows a comparison of plaque forming cells comparing T cell helper clone 7A1 and murine EL40.9 cells which secrete a soluble CD40-L. The EL40.9 cells seem to have an inhibitory effect upon antigen specific antibody formation. Figure 11 shows PFC (plaque forming cells) for T cell helper cells 7C2 and CV1 EBNA cells transfected with either empty vector or CD40-L. Both 7C2 cells and membrane-bound CD40-L stimulated antigen specific antibody formation (PFC). Figure 13 compares antigen specific antibody formation of CD40-L and 7A1 cells in the presence or absence of 10 ng/ml interleukin-2 (IL-2). IL-2 increased PFC for 7A1 cells but did not increase PFC caused by membrane-bound CD40-L.

Polyclonal Ig production by murine B cells was compared for stimulation or inhibition with membrane-bound CD40-L, control CV1 EBNA cells and helper T cells 7A1 in the presence of cytokines IL-4 (10 ng/ml) and IL-5 (1:40 dilution of COS cell supernatants) or without added cytokines. The amount of IgA, IgG3, IgE, IgG2b, IgM and IgG1 are shown in Tables 3-8, respectively.

TABLE 3

IgA, ng/ml

| | # CELLS | MEDIA | +IL-4+IL-5 |
|--------------|-----------|-------------------|--------------------|
| CD40-L | 2 X 10(5) | 666.275 ± 174.444 | 64.639 ± 51.780 |
| | 1 X 10(5) | 288.085 ± 20.773 | 291.831 ± 10.673 |
| | 1 X 10(4) | 53.750 ± 36.531 | 910.072 ± 62.713 |
| HAVEO | 2 X 10(5) | 0 | 628.190 ± 42.907 |
| | 1 X 10(5) | 0 | 477.755 ± 57.478 |
| | 1 X 10(4) | 0 | 295.640 ± 12.736 |
| 7A1 (2C11) | 1 X 10(6) | 0 | 2177.549 ± 377.052 |
| | 2 X 10(5) | 0 | 646.898 ± 86.325 |
| | 1 X 10(5) | 0 | 480.671 ± 40.011 |
| MEDIA LPS | | 0 | 458.152 ± 77.258 |
| | | 88.531 ± 31.248 | 132.336 ± 51.356 |

TABLE 4

IgG3, ng/ml

| | | # CELLS | MEDIA | +IL-4+IL-5 |
|----|------------|-----------|------------------|------------------|
| 5 | | | | |
| | CD40-L | 2 X 10(5) | 108.427 ± 14.359 | 0 |
| | | 1 X 10(5) | 118.079 ± 8.021 | 46.535 ± 9.899 |
| 10 | | 1 X 10(4) | 127.591 ± 6.268 | 467.023 ± 78.276 |
| | HAVEO | 2 X 10(5) | 0 | 29.773 ± 5.224 |
| | | 1 X 10(5) | 11.205 ± 4.434 | 66.323 ± 8.673 |
| | | 1 X 10(4) | 26.389 ± 10.221 | 34.671 ± 12.975 |
| 15 | | | | |
| | 7A1 (2C11) | 1 X 10(6) | 33.420 ± 9.972 | 820.856 ± 39.442 |
| | | 2 X 10(5) | 0 | 436.074 ± 59.332 |
| | | 1 X 10(5) | 0 | 239.760 ± 45.978 |
| 20 | | | | |
| | MEDIA | | 21.808 ± 7.107 | 64.773 ± 13.924 |
| | LPS | | 816.697 ± 43.553 | 103.720 ± 11.883 |

TABLE 5

IgE, ng/ml

| | | # CELLS | MEDIA | +IL-4+IL-5 |
|----|------------|-----------|-------|------------------|
| | | | | |
| | CD40-L | 2 X 10(5) | 0 | 64.144 ± 4.979 |
| | | 1 X 10(5) | 0 | 83.493 ± 9.093 |
| | | 1 X 10(4) | 0 | 461.155 ± 60.514 |
| | HAVEO | 2 X 10(5) | 0 | 0 |
| | | 1 X 10(5) | 0 | 4.208 ± .527 |
| 40 | | 1 X 10(4) | 0 | 0 |
| | 7A1 (2C11) | 1 X 10(6) | 0 | 208.091 ± 8.090 |
| | | 2 X 10(5) | 0 | 32.530 ± 0.723 |
| | | 1 X 10(5) | 0 | 15.889 ± 2.947 |
| 45 | | | | |
| | MEDIA | | 0 | 12.602 ± 1.460 |
| | LPS | | 0 | 408.355 ± 9.764 |

TABLE 6

IgG2b, ng/ml

| 5 | | # CELLS | MEDIA | +IL-4+IL-5 |
|----|------------|-----------|-------|-----------------|
| | CD40-L | 2 X 10(5) | 0 | 0 |
| | | 1 X 10(5) | 0 | 6.230 ± .285 |
| 10 | | 1 X 10(4) | 0 | 47.414 ± .241 |
| | HAVEO | 2 X 10(5) | 0 | 7.001 ± 2.358 |
| | | 1 X 10(5) | 0 | 6.230 ± 2.285 |
| | | 1 X 10(4) | 0 | 9.620 ± 2.650 |
| 15 | 7A1 (2C11) | 1 X 10(6) | 0 | 189.343 ± 2.837 |
| | | 2 X 10(5) | 0 | 22.431 ± 6.835 |
| | | 1 X 10(5) | 0 | 7.207 ± 1.580 |
| 20 | MEDIA | | 0 | 7.422 ± 1.602 |
| | LPS | | 0 | 33.291 ± 3.183 |

TABLE 7

IgM, µg/ml

| 30 | | # CELLS | MEDIA | +IL-4+IL-5 |
|----|------------|-----------|----------------|------------------|
| | CD40-L | 2 X 10(5) | 1.805 ± 0.639 | 0.439 ± 0.184 |
| | | 1 X 10(5) | 2.237 ± 0.583 | 5.878 ± 0.858 |
| 35 | | 1 X 10(4) | 2.293 ± 0.595 | 96.730 ± 13.009 |
| | HAVEO | 2 X 10(5) | 0 | 10.890 ± 2.126 |
| | | 1 X 10(5) | 0 | 13.303 ± 0.993 |
| | | 1 X 10(4) | 0.624 ± 0.178 | 22.538 ± 2.304 |
| 40 | 7A1 (2C11) | 1 X 10(6) | 0.769 ± 0.124 | 104.857 ± 17.463 |
| | | 2 X 10(5) | 0.142 ± 0.052 | 27.016 ± 1.706 |
| | | 1 X 10(5) | 0.126 ± 0.048 | 13.070 ± 0.600 |
| 45 | MEDIA | | 0.231 ± 0.057 | 36.809 ± 2.860 |
| | LPS | | 53.302 ± 9.668 | 41.974 ± 6.158 |

TABLE 8

IgG1, ng/ml

| 5 | | # CELLS | MEDIA | +IL-4+IL-5 |
|----|------------|-----------|-------|-------------------|
| | CD40-L | 2 X 10(5) | 0 | 130.185 ± 24.547 |
| | | 1 X 10(5) | 0 | 310.588 ± 1.261 |
| 10 | | 1 X 10(4) | 0 | 270.727 ± 17.511 |
| | HAVEO | 2 X 10(5) | 0 | 187.668 ± 57.730 |
| | | 1 X 10(5) | 0 | 43.320 ± 49.770 |
| | | 1 X 10(4) | 0 | 1363.464 ± 45.841 |
| 15 | 7A1 (2C11) | 1 X 10(6) | 0 | 145.652 ± 136.070 |
| | | 2 X 10(5) | 0 | 365.563 ± 24.276 |
| | | 1 X 10(5) | 0 | 449.475 ± 101.012 |
| 20 | MEDIA | | 0 | 133.660 ± 386.231 |
| | LPS | | 0 | 246.213 ± 21.526 |

These data indicate that the interaction of CD40 with its ligand is the principal molecular interaction responsible for T cell contact dependent induction of B cell growth and differentiation to both antigen-specific antibody production and polyclonal Ig secretion. As such, these data suggest that antagonists of this interaction, by soluble CD40, CD40/Fc fusion protein and possibly soluble CD40-L (monomeric), will significantly interfere with development of antibody responses. Therefore clinical situations where CD40, CD40/Fc fusion proteins and soluble CD40-L include allergy, lupus, rheumatoid arthritis, insulin dependent diabetes mellitus, and any other diseases where autoimmune antibody or antigen/antibody complexes are responsible for clinical pathology of the disease. Moreover, membrane-bound CD40-L or oligomeric soluble CD40-L will be useful to stimulate B cell proliferation and antibody production. As such, these forms of CD40-L are most useful for vaccine adjuvants and as a stimulating agent for mAb secretion from hybridoma cells.

EXAMPLE 13

This example illustrates the effect of membrane-bound CD40-L upon proliferation of and IgE secretion from peripheral blood mononuclear cells (E⁻). E⁻ cells were obtained according to the procedure described in Example 10 and incubated for 7 or 10 days in the presence of CV1 EBNA cells transfected with empty vector or mCD40-L cDNA. Additionally, CD40/Fc fusion protein (described in Example 1) or TNF Receptor/Fc fusion protein (described in WO 91/03553) was added to some of the preparations as indicated in Figure 14. IgE secretion was measured according to the procedure described in Example 8 and B cell proliferation was measured according to the procedure described in Example 10.

The results for B cell proliferation and IgE secretion are shown in Figure 14 for five different concentrations of transfected CV1 EBNA cells. Both B cell proliferation and IgE secretion were increased in the presence of membrane-bound CD40-L. Addition of CD40/Fc fusion protein ablated both B cell proliferation and IgE secretion. The TNF Receptor/Fc fusion protein had no effect. As a comparison for IgE secretion, addition of IL-4 as a control agent (without transfected CV1 EBNA cells) produced no IgE in this assay and addition of IL-4 plus G28-5 anti-CD40 mAb resulted in 29.7 ng/ml IgE in this assay.

EXAMPLE 14

This example describes construction of a CD40-L/Fc DNA construct to express a soluble CD40-L/Fc fusion protein referred to as CD40-L/FC2 construct. DNA encoding CD40-L/FC2 comprises sequences encoding a leader (or signal) peptide, an eight amino acid hydrophilic sequence described by Hopp et al. (Hopp et al., *Bio/Technology* 6:1204,1988; referred to as Flag[®]), a suitable Fc region of an immunoglobulin, a [Gly₄Ser]₃ repeat sequence (described in U.S. Patent 5,073,627, which is incorporated by reference herein) or other suitable linker sequence, and the extracellular region of human CD40-L from amino acid 50 to amino acid 261 (SEQ ID NO:11). A pDC406 expression vector containing a leader sequence, Flag[®], and human IgG₁ Fc is prepared using conventional techniques of enzyme cutting and ligation of fragments encoding a leader sequence, Flag[®], and human IgG₁ Fc, and restricted with *Nsi* 1 and *Not* 1.

A PCR technique (Saiki et al., *Science* 239:487, 1988) was employed using 5' (upstream) and 3' (downstream) oligonucleotide primers to amplify the DNA sequences encoding CD40 extracellular ligand binding domain from a cloning vector containing human CD40-L (ATCC 68873; SEQ ID NO: 11) to form a PCR fragment. The upstream oligonucleotide primer (SEQ ID NO:13) introduced a *Nsi* 1 site upstream from a linker sequence ([Gly₄Ser]₃SerSer), which was followed by 21 nucleotides of the extracellular domain of CD40-L (amino acids 51 through 57 of SEQ ID NO: 11). A downstream oligonucleotide primer (SEQ ID NO:14) introduced a *Not* 1 site just downstream of the termination codon of the CD40-L. The PCR fragment was then ligated into the pDC406 expression vector containing a leader sequence, Flag[®], and human IgG₁ Fc. The nucleotide and predicted amino acid sequence of CD40-L/FC2 are presented in SEQ ID NO:15 and SEQ ID NO:16. The resultant DNA construct (CD40-L/FC2) was transfected into the monkey kidney cell line CV-1/EBNA (ATCC CRL 10478). The construct encoded a soluble CD40-L capable of binding CD40, as evidenced by binding observed in fluorescence-activated cell sorting (FACS) analysis using cells that express CD40.

Large scale cultures of human embryonic kidney 293 cells (ATCC CRL 1573) transfected with the construct encoding CD40-L/FC2 were grown to accumulate supernatant containing CD40-L/FC2. The 293 cell line, a permanent line of primary human embryonal kidney transformed by human adenovirus 5 DNA, permits expression of recombinant proteins

ligated into the pCD406 vector. The CD40-L/FC2 fusion protein in supernatant fluid was purified by affinity purification. Briefly, culture supernatant containing the CD40-L/FC2 fusion protein was purified by filtering mammalian cell supernatants (e.g., in a 0.45µ filter) and applying filtrate to an antibody affinity column comprising biotinylated goat anti-human IgG (Jackson ImmunoResearch Laboratories, Inc., Westgrove, PA, USA) coupled to Streptavidin-agarose (Pierce Chemical, Rockford, IL, USA) at 4°C, at a flow rate of approximately 60 to 80 ml/hr for a 1.5 cm x 12.0 cm column. The column was washed with approximately 20 column volumes of PBS (phosphate buffered saline), until free protein could not be detected in wash buffer. Bound fusion protein was eluted from the column with 12.5 mM citrate buffer, 75 mM NaCl, pH 2.8, and brought to pH 7 with 500 mM Hepes buffer, pH 9.1. The purified, oligomeric CD40-L/FC2 peptide induced human B cell proliferation in the absence of any co-stimuli, and (in conjunction with the appropriate cytokine) resulted in the production of IgG, IgE, IgA and IgM, as described in Example 12 for membrane-bound CD40-L.

EXAMPLE 15

This example describes construction of a CD40-L DNA construct to express a soluble CD40-L fusion protein referred to as trimeric CD40-L. Trimeric CD40-L contains a leader sequence, a 33 amino acid sequence referred to as a "leucine zipper" (SEQ ID NO:17), and an eight amino acid hydrophilic sequence described by Hopp et al. (Hopp et al., *Bio/Technology* 6:1204,1988; referred to as Flag®), followed by the extracellular region of human CD40-L from amino acid 50 to amino acid 261 (SEQ ID NO:11). The utility of the leader and the Flag® sequences have been described in the Detailed Description. The 33 amino acid sequence presented in SEQ ID NO:17 trimerizes spontaneously in solution. Fusion proteins comprising this 33 amino acid sequence are thus expected to form trimers or multimers spontaneously.

The construct is prepared by synthesizing oligonucleotides representing a leader sequence, the 33 amino acid sequence described above, and the Flag® sequence, then ligating the final product to a DNA fragment encoding amino acids 51 through 261 of SEQ ID NO:11, prepared as described in Example 14.

The resulting ligation product in expression vector pDC406 was transfected into the monkey kidney cell line CV-1/EBNA (ATCC CRL 10478). The pDC406 plasmid includes regulatory sequences derived from SV40, human immunodeficiency virus (HIV), and Epstein-Barr virus (EBV). The CV-1/EBNA cell line was derived by transfection of the CV-1 cell line with a gene encoding Epstein-Barr virus nuclear antigen-1 (EBNA-1) that constitutively expresses EBNA-1 driven from the human CMV intermediate-early enhancer/promoter. The EBNA-1 gene allows for episomal replication of expression vectors, such as pDC406, that contain the EBV origin of replication.

Once cells expressing the fusion construct are identified, large scale cultures of transfected cells are grown to accumulate supernatant from cells expressing trimeric CD40-L.

The trimeric CD40-L fusion protein in supernatant fluid is purified by affinity purification substantially as described in U.S. Patent 5,011,912. Silver-stained SDS gels of the eluted CD40-L fusion protein can be prepared to determine purity.

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EXAMPLE 16

This example describes two solid-phase binding assays, the first of which, (a), can be used to assess the ability of trimeric CD40-L to bind CD40, and the second of which, (b), is used to detect the presence of CD40-L.

(a) Quantitative CD40-L ELISA

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CD40/Fc is prepared and purified as described Example 1, and used to coat 96-well plates (Corning EasyWash ELISA plates, Corning, NY, USA). The plates are coated with 2.5 µg/well of CD40/Fc in PBS overnight at 4°C, and blocked with 1% non-fat milk in PBS for 1 hour at room temperature. Samples to be tested are diluted in 10% normal goat serum in PBS, and 50 µl is added per well. A titration of unknown samples is run in duplicate, and a titration of reference standard of CD40-L is run to generate a standard curve. The plates are incubated with the samples and controls for 45 minutes at room temperature, then washed four times with PBS. Second step reagent, rabbit anti leucine zipper, is added (50 µl/well, concentration approximately 2.5 µg/ml), and the plates are incubated at room temperature for 45 minutes. The plates are again washed as previously described, and goat F(ab')₂ anti-rabbit IgG conjugated to horseradish peroxidase (Tago, Burlingame, CA, USA) is added. Plates are incubated for 45 minutes at room temperature, washed as described, and the presence of CD40-L is detected by the addition of chromogen, tetramethyl benzidine (TMB; 100µl/well) for 15 minutes at room temperature. The chromogenic reaction is stopped by the addition of 100 µl/well 2N H₂SO₄, and the OD₄₅₀-OD₅₆₂ of the wells determined. The quantity of trimeric CD40-L can be determined by comparing the OD values obtained with the unknown samples to the values generated for the standard curve. Values are expressed as the number of binding units per ml. A binding unit is roughly one ng of protein as estimated using a purified Fc fusion protein of the ligand as a standard. In this manner, the concentration and specific activity of several different batches of trimeric CD40-L purified as described in Example 19 have been determined.

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(b) Qualitative Dot Blot

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CD40-L trimer (1 µl of crude supernatant or column fractions) is adsorbed to dry BA85/21 nitrocellulose membranes (Schleicher and Schuell, Keene, NH) and allowed to dry. The membranes are incubated in tissue culture dishes for one hour in Tris (0.05 M) buffered saline (0.15 M) pH 7.5 containing 1% w/v BSA to block nonspecific binding sites. At the end of this time, the membranes are washed three times in PBS, and rabbit anti-leucine zipper antibody is added at an approximate concentration of 10 µg/ml in PBS containing 1% BSA, following which the membranes are incubated for one hour at room temperature. The membranes are again washed as described, and a horseradish peroxidase (HRP)-labeled

antibody (such as goat anti-rabbit Ig; Southern Biotech, Birmingham, AL) at an approximate dilution of 1:1000 in PBS containing 1% BSA is added. After incubating for one hour at room temperature, the membranes are washed and chromogen (i.e. 4-chloronaphthol reagent, Kirkegard and Perry, Gaithersburg, MD) is added. Color is allowed to develop for ten minutes at room temperature, and the reaction is stopped by rinsing the membranes with water. The membranes are washed, and the presence of CD40-L is determined by analyzing for the presence of a blue-black color. This assay was used to determine the presence or absence of trimeric CD40-L in cell culture supernatant fluids and in purification column fractions. The assay further provides a semi-quantitative method of determining relative amounts of trimeric CD40-L by comparing the intensity of the color in unknown samples to the intensity of known quantities of controls.

EXAMPLE 17

This example describes construction of a human CD40-L DNA construct to express trimeric CD40-L in Chinese hamster ovary (CHO) cells. As described in Example 15, trimeric CD40-L contains a leader sequence, and a 33 amino acid sequence referred to as a "leucine zipper" (SEQ ID NO:17), followed by the extracellular region of human CD40-L from amino acid 51 to amino acid 261 (SEQ ID NO:11). The construct was prepared by cutting the appropriate DNA from the a plasmid containing human CD40-L (derived from the plasmid described in Example 15), and ligating the DNA into the expression vector pCAVDHFR. The resultant construct was referred to as CAV/DHFR-CD40LT. pCAVDHFR includes regulatory sequences derived from cytomegalovirus, SV40, and Adenovirus 2, along with the gene for dihydrofolate reductase (DHFR), and allows random integration of a desired gene into host cell chromosomes. Expression of DHFR enables the DHFR⁻ host cells to grow in media lacking glycine, hypoxanthine, and thymidine (GHT). A similar construct was also made for expression of murine CD40-L timer in CHO cells. In addition to the leader and leucine zipper sequences, the murine construct also contained a sequence encoding the octapeptide referred to as Flag® (described previously) between the trimerization domain (leucine zipper) and the extracellular region of murine CD40-L. The nucleotide and amino acid sequence of the human and murine trimeric CD40-L-encoding DNAs are shown in SEQ ID NOs 20 and 22 respectively. Additional constructs can be prepared using standard methods. For example, vectors which incorporates dual promoters such as those described in U.S. Patent 4,656,134, or vectors employing enhancer sequences such as those described in U.S. Patent 4,937,190 or in Kaufman et al., *Nucl. Acids Res.* 19:4485, 1991, are also useful in preparing constructs for expression of CD40-L in CHO cells.

The resulting ligation product was transfected into CHO cells using either Lipofectin® Reagent or Lipofectamine™ Reagent (Gibco BRL, Gaithersburg, MD). Both of these reagents are commercially available reagents used to form lipid-nucleic acid complexes (or liposomes)

which, when applied to cultured cells, facilitate uptake of the nucleic acid into the cells. Cells which were transfected with the pCAVDHFR-CD40LT construct were selected in DMEM:F12 medium in the absence of GHT. Cells which were able to grow in the absence of GHT were tested for production of CD40-L using a solid phase binding assay as described in Example 16. Results indicated that in this transfection system, Lipofectamine™ Reagent gave higher rates of successful transfection.

Approximately 160 clones were screened and two positive clones were identified and expanded for further study. Cells were passaged in GHT-free DMEM:F12 medium, and monitored for stability by assessing production of trimeric CD40-L in the solid-phase binding assay described above. Based on these results, one clone was chosen which appeared to be stably transfected with the CD40-L DNA, and which produced and secreted approximately 1 µg/10⁶ cells/day of CD40-L trimer. Additional constructs comprising other vectors and all or a portion of the DNA sequences described in this example can be used to prepare additional stably transfected cell lines, substantially as described herein. For example, constructs encoding monomeric CD40-L similar to those described in Example 18 can be prepared, as can plasmids encoding any of the previously described constructs.

Once such stably transfected cells were identified, large scale cultures of transfected cells were grown to accumulate supernatant containing trimeric CD40-L. Suitable large-scale culture conditions include the use of bioreactors, as described below in Example 19. Similar procedures were followed to produce CHO cell lines that secreted a trimeric murine CD40-L at approximately 0.05 µg/10⁶ cells/day. CHO cells stably transfected with either the human or murine CD40-L construct, having acquired a DHFR gene from the pCAVDHFR plasmid, are resistant to methotrexate. Methotrexate can be added to the culture medium to amplify the number of copies of the CD40-L trimer DNA in order to increase production of CD40-L trimer.

EXAMPLE 18

This example describes construction of a murine CD40-L DNA construct to express a soluble CD40-L protein referred to as monomeric CD40-L. Monomeric CD40-L contains a leader sequence, an eight amino acid sequence referred to as Flag® (amino acids 1-8 of SEQ ID NO:16), followed by the amino terminal truncated region of CD40-L encompassing the extracellular B-sheet forming region of the CD40 molecule from amino acid 119 to 260 of SEQ ID NO:1. A 68 amino acid stretch of the extracellular spacer region of the CD40-L molecule (amino acids 51-118 of SEQ ID NO:1) has been deleted in this construct, as has the transmembrane region (amino acids 1-50 of SEQ ID NO:1).

A PCR technique using 5' (upstream) and 3' (downstream) oligonucleotide primers was used to amplify the DNA sequences encoding the CD40-L truncated extracellular domain from a cloning vector containing murine CD40-L. The upstream oligonucleotide primer (ATATGAATTCTGACTACAAAGATGACGATGATAAACCTCAAATTGCAGCACACGTT; SEQ ID NO:18) appended an EcoRI site and the Flag coding sequence upstream from CD40 nucleotide 355.

The downstream oligonucleotide primer (CCTTCGCGGCCGCGTTCAGAGTTT GAGTAAGCCAA, SEQ ID NO:19) introduced a Not I site downstream of the authentic termination codon of the CD40L.

The PCR fragment was ligated into the multiple cloning site (EcoRI/NotI) of the baculovirus expression vector pAcGP67A (PharMingen, San Diego, CA) which contains the signal sequence for a glycoprotein of the Autographica californica nuclear polyhedrosis virus under the control of the viral polyhedrin promoter. The resultant DNA construct was cotransfected with Autographica californica viral DNA into *Spodoptera frugiperda* cells (SF21), and the resultant recombinant virus was plaque purified.

The CD40-L protein encoded by this construct was purified by Flag® affinity chromatography from serum free culture of recombinant virus infected cells. Purified protein had an apparent molecular weight of 21Kd when run in a reducing PAGE and stained with Coomassie Blue. Both crude infected cell supernatants containing CD40-L and affinity purified CD40-L protein showed receptor binding activity in a solid phase assay utilizing the CD40Fc recombinant receptor. Mock infected controls had no activity.

A similar CD40-L construct was made without an amino terminal Flag® sequence. This construct utilized an existing Bam HI site at nucleotide 351 in the CD40-L sequence and the downstream PCR oligonucleotide primer described above (SEQ ID NO:19). After amplification of the CD40 sequence with a 5' upstream oligonucleotide homologous to CD40-L nucleotides 324-346, and the downstream primer which introduced a Not I site, the PCR product was cut with Bam HI and Not I and ligated into pAcGP67A cut with Bam HI and NotI. This construct was cotransfected into SF21 cells along with viral DNA as previously described, and recombinant virus was plaque purified, expanded and used to infect insect cells to produce serum free conditioned supernatants. CD40-L was detectable in these crude supernatants by both CD40Fc receptor binding assay and by detection of an 18 Kd band on a Coomassie Blue-stained PAGE.

EXAMPLE 19

This example describes purification of trimeric murine CD40L from supernatant fluid from transfected CHO cells. A CHO cell line expressing muCD40LT was maintained in suspension in spinner-flask cultures. For production, the cells were centrifuged and resuspended into a controlled 3 liter bioreactor in serum-free medium. Oxygen, agitation and pH were controlled for at 40% dissolved O₂ (relative to air saturation), 150 RPM and 7.2, respectively. The culture was harvested after nine days. A total volume of approximately 160 ml of supernatant fluid from the bioreactor was dialyzed overnight at 4°C against 4 L of 20 mM Tris pH 7.5 buffer containing 150mM NaCl, and then adjusted to 1M (NH₄)₂SO₄ by the addition of solid (NH₄)₂SO₄. Dialysis accomplished the removal of low-molecular weight contaminants; other techniques will also be useful for this purpose, for example, constant volume diafiltration.

The dialyzed supernatant was initially purified by hydrophobic interaction chromatography. The supernatant was applied to a 1.6 x 13 cm (26 ml) Phenyl Sepharose® CL-4B column (Pharmacia, Uppsala, Sweden) previously equilibrated with 10 mM Tris pH 8.0/1M (NH₄)₂SO₄ (Buffer A). The column was washed with 60 mL Buffer A, and bound proteins were eluted at 2 mL/min with a decreasing (NH₄)₂SO₄ gradient using Buffer A and 10 mM Tris pH 8.0 (Buffer B). The gradient conditions were 0 to 60% Buffer B in 20 ml, hold at 60% Buffer B for 60 ml, 60 to 100% Buffer B in 20 ml, and hold at 100% Buffer B for 60 ml. A total of 53 3 ml fractions were collected during the elution process. The elution of protein was monitored by absorbance at 280 nm. The presence of active trimeric CD40L was determined by an ELISA as described in Example 16. A peak of activity eluted in fractions 8 - 20. In a subsequent purification run, highsub and lowsub Phenyl Sepharose 6 Fast Flow (Pharmacia, Uppsala, Sweden) were used for the hydrophobic interaction step; the highsub Phenyl Sepharose column was found to give equivalent results to those obtained with Phenyl Sepharose® CL-4B.

Peak fractions from the Phenyl Sepharose® CL-4B column were pooled, and glycerol was added to a final concentration of 10% (v/v). The pool was then concentrated to a volume of approximately 4.5 ml using Amicon Centriprep 10 concentrators with a 10,000 molecular weight cutoff, and chromatographed over a sizing column (Superdex 200 26/60; Pharmacia, Uppsala, Sweden; 2.6 x 60 cm). The concentrated pool was loaded, and eluted with 20 mM Tris pH 7.5/150mM NaCl/10 % glycerol (v/v), at a flow rate of 2.0 ml/min. Protein elution was monitored at 280 nm, and eighty 2 ml fractions were collected. Activity was determined as described above; a peak of activity eluted in fractions 36 - 48. Purity was evaluated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) under reducing conditions on 10% acrylamide gels (Novex). The gels were stained by silver stain substantially as described by Oakley et al., *Anal. Biochem.* 105:361 (1980). The silver-stained gels showed several proteins present in the fractions.

Fractions from the peak of activity from the Superdex 200 column were pooled, concentrated as described above to approximately 2.0 ml, diluted 1:2 in 20 mM Bis Tris Propane pH6.5/10 % glycerol (v/v), and further purified by anion exchange chromatography. The concentrated pooled material was applied at 1 mL/min to a Mono Q column (Pharmacia, 0.5 x 5 cm) equilibrated with 20 mM Bis Tris Propane pH6.5/10 % glycerol (v/v) (Buffer A). The column was washed with 16 mL Buffer A and eluted with a salt gradient using Buffer A and 20 mM Bis Tris Propane pH6.5/500 mM NaCl/10 % glycerol (v/v) (Buffer B). The column elution conditions were 0 to 60% Buffer B in 20 ml, 60 to 100% Buffer B in 1.0 ml, and hold at 100% Buffer B for 10 ml. A total of 30 1 ml fractions were collected during the elution process. Activity and A₂₈₀ were monitored as described previously. A peak of activity eluted in fractions 15 - 23. The fractions were evaluated by SDS-PAGE and silver stain as described above. Fractions 20 - 22 were estimated to contain about 80% trimeric murine CD40L, and were pooled. In a subsequent run, a High-performance Q resin (Pharmacia,

Uppsala, Sweden) was used and found to give equivalent results. Table 9 below summarizes the results of the procedure used to purify trimeric murine CD40L.

Table 9: Purification of Trimeric Murine CD40-L

| Step | Volume (ml) | Total # Binding Units | Total Protein (mg) | Specific Activity * |
|--------------------------|-------------|-----------------------|--------------------|---------------------|
| 1. Supernatant fluid | 160 | 5.2×10^6 | 280 | 1.9×10^4 |
| 2. Dialyzed Supernatant | 169 | 6.4×10^6 | 106 | 6.0×10^4 |
| 3. Phenyl Sepharose pool | 37 | 2.3×10^6 | 8.0 | 2.9×10^5 |
| 4. Superdex 200 pool | 24 | 2.3×10^6 | 1.4 | 1.6×10^5 |
| 5. Mono Q pool | 7 | 6.4×10^5 | 0.91 | 7.0×10^5 |

- 5 * Specific activity is defined as the number of binding units of CD40-L per mg protein. One binding unit of CD40L is defined as 0.5 ng of purified CD40-L, as determined in a quantitative, enzyme-based binding assay. Protein concentration was determined using the BCA Protein Assay Reagent (Pierce); bovine serum albumen was used as the standard.

EXAMPLE 20

This example describes the effect of CD40-L trimer (CD40LT) on primary antibody response to a T-dependent antigen. On day 0, 6 BALB/c mice were injected subcutaneously with 200µl of a suspension containing 10 µg of ovalbumen (OVA), in the presence of Freund's incomplete adjuvant (IFA). Three of the mice also received 200µl of PBS containing a total of 1.5 µg CD40LT, while the remaining mice received a similar amount of a control protein (murine serum immunoglobulin; msIgG). The mice were again treated with 1.5 µg of CD40LT or control protein on day 6.

Serum samples were taken on days 7 and 14, and analyzed for elevated levels of antigen-specific IgG or IgM using an OVA ELISA. Briefly, 96-well plates were coated with 10µg/well of OVA at 4°C overnight, then blocked with non-fat milk. Serial two-fold dilutions of serum samples were prepared in PBS containing 10% normal goat serum, and 50µl of each dilution was added to a well. Plates were incubated for one hour at room temperature, and washed with PBS. The presence of antigen-specific IgG or IgM was detected using goat anti mouse IgG or IgM (Southern Biotech) conjugated to horseradish peroxidase for one hour at room temperature, followed by a wash step and the addition of substrate (TMB, Kirkegard and Perry). Color development proceeded for ten minutes at room temperature, and was stopped by the addition of H₂SO₄. The maximal dilution of serum dilution containing IgG or IgM anti-OVA activity was determined by plotting the OD₄₅₀-OD₅₆₂ of the diluted mouse sera, and comparing the OD values obtained with OD values from pre-immune sera. Results are presented in Table 10 below.

Table 10: Effect of Trimeric Murine CD40-L on Primary Immune Response

| Treatment: | Total IgG ^a | | Relative Ab levels ^b | |
|-------------|------------------------------------|--------|----------------------------------|--------|
| | Endpoint titer (est ^c) | | % over non-immune _{max} | |
| | Day 7 | Day 14 | Day 7 | Day 14 |
| msIgG (#1) | <50 | 400 | <25 | 216 |
| msIgG (#2) | <50 | >400 | <25 | 285 |
| msIgG (#3) | <50 | 200 | <25 | 212 |
| CD40LT (#1) | 400 | 200 | 279 | 240 |
| CD40LT (#2) | 800 | >400 | 379 | 339 |
| CD40LT (#3) | 200 | 200 | 178 | 228 |

a: Antigen-specific IgM titers were low at both day 7 and day 14 in both groups.

b: (OD_{max} of treated mouse/OD_{max} of pre-immune control) X 100

c: Estimated.

The mice treated with CD40LT exhibited greater levels of OVA-specific IgG as compared to control mice, indicating that CD40LT was able to boost a primary immune response to a T-dependent antigen, both enhancing the level of antigen-specific antibody and isotype switching from IgM to IgG.

A second experiment was carried out using different lots of reagents and varying the concentrations of the CD40-L. A significant difference between the control mice and the mice treated with CD40 ligand was not observed at day 7, however, CD40-L did enhance the day 14 response. Additional experiments to address the use of CD40-L will include an analysis of different antigens as well as the use of different adjuvants and delivery systems.

EXAMPLE 21

This example illustrates the activities of monoclonal antibodies to CD40-L. Supernatants from 264 hybridomas prepared as described in Example 7 were screened for anti-CD40-L activity by FACS analysis using human peripheral blood T cells stimulated with PMA and ionomycin for 16 hours. Under these conditions, four of the tested hybridoma supernatants gave a FACS profile similar to that obtained with CD40/Fc; an exemplary FACS profile is shown in Figure 15. Six additional hybridoma supernatants gave weak positive results, and the remainder did not appear to bind activated T cells.

The ten hybridoma supernatants that gave positive or weak positive results were then tested in another FACS assay using CV-1/EBNA cells transfected with vector alone or with vector encoding human CD40-L, as well as being reevaluated against activated T cells. Several of the supernatants appeared to be non-specifically reactive, however, three supernatants specifically stained CD40-L expressing CV-1/EBNA cells, and were selected for cloning and further evaluation.

The three anti-CD40-L secreting clones were expanded and supernatant fluids were evaluated for ability to bind CD40-L and inhibit (or block) binding of CD40-L to CD40. In a

FACS assay using activated human T cells (prepared as described above), the monoclonal antibody secreted by three of the clones blocked the binding of CD40/Fc to CD40-L, whereas the fourth did not. Representative results are shown in Figure 16. Several of the monoclonal antibodies were also tested for the ability to inhibit B cell proliferation in an assay substantially as described in Example 13 herein, using CD40-L-containing supernatant fluid from COS cells transfected with a vector encoding CD40-L. As shown in Figure 17, the monoclonal antibodies that were able to inhibit binding of CD40/Fc to CD40-L by FACS analysis also inhibited the ability of trimeric CD40-L plus anti-IgM to induce proliferation of peripheral blood B cells.

The monoclonal antibodies were also evaluated in a solid phase ELISA in which plates were coated with a rabbit antibody to the leucine zipper domain of trimeric CD40-L. Trimeric CD40-L was then added to the plates, followed by (after appropriate incubation and washing steps) supernatant fluids containing the monoclonal antibodies. The presence of antibodies to the CD40-L trimer was detected using enzyme labeled anti-mouse immunoglobulin followed by the appropriate substrate. The three monoclonal antibodies that inhibited the binding of CD40/Fc to CD40-L expressing T cells by FACS also bound to the CD40-L trimer used in the solid phase ELISA. Two of the hybridoma cell lines (designated M90 and M91) were selected for further expansion. These hybridoma cell have been deposited with the American Type Culture Collection under terms of the Budapest treaty on _____, and given accession number _____ (M90) and _____ (M91).

EXAMPLE 22

This example illustrates the binding affinities of several different CD40-L constructs. Affinity experiments were conducted by biospecific interaction analysis (BIA) using a biosensor, an instrument that combines a biological recognition mechanism with a sensing device or transducer. An exemplary biosensor is BIAcore™, from Pharmacia Biosensor AB (Uppsala, Sweden; see Fägerstam L.G., *Techniques in Protein Chemistry II*, ed. J.J. Villafranca, Acad. Press, NY, 1991). BIAcore™ uses the optical phenomenon surface plasmon resonance (Kretschmann and Raether, *Z. Naturforschung, Teil. A* 23:2135, 1968) to monitor the interaction of two biological molecules. Molecule pairs having affinity constants in the range 10^5 to 10^{10} M⁻¹, and association rate constants in the range of 10^3 to 10^6 M⁻¹s⁻¹, are suitable for characterization with BIAcore™.

The biosensor chips were coated with goat anti-human IgG₁ Fc, which was used to bind CD40/Fc (prepared as described in Example 1) to the chip. The different constructs of CD40-L were then added at increasing concentrations; the chip was regenerated between the different constructs by the addition of sodium hydroxide. Two separate experiments were performed. In the first, the binding of a dimeric human CD40-L (Example 14), trimeric human CD40-L (Example 15), dimeric murine CD40-L (prepared substantially as described in Example 14 for human CD40-L/Fc) and trimeric murine CD40-L (prepared substantially as

described for the human CD40-L in Example 15) were compared. In the second experiment, the binding of trimeric human CD40-L was compared to the binding of two different preparations of monomeric human CD40-L prepared as described in Example 18. The resultant data were analyzed to determine the affinity and association rate constants of the different CD40-L constructs. Results are shown in Table 12 below, and in Figures 18 and 19.

Table 12: Binding of CD40-L to CD40/Fc

| | Site 1 (mol/mol CD40/Fc) | K ₁ (M ⁻¹) | Site2 (mol/mol CD40/Fc) | K ₂ (M ⁻¹) |
|---------------|-----------------------------|--------------------------------------|----------------------------|--------------------------------------|
| Human Trimer | 0.04 ± 0.02 | 5 ± 3 × 10 ⁹ | 0.68 ± 0.07 | 7.5 ± 2.5 × 10 ⁷ |
| Human Dimer | 0.013 ± 0.002 | 1.6 ± 0.7 × 10 ¹¹ | 0.049 ± 0.004 | 7.0 ± 2.1 × 10 ⁸ |
| Murine Trimer | 0.02 ± 0.003 | 6 ± 3 × 10 ¹⁰ | 0.44 ± 0.02 | 1.6 ± 0.2 × 10 ⁸ |
| Murine Dimer | 0.05 ± 0.02 | 7 ± 4 × 10 ⁹ | 0.14 ± 0.23 | 4.0 ± 1.0 × 10 ⁷ |
| Human Trimer | 0.26 | 6.6 × 10 ⁸ | 0.41 | 2.6 × 10 ⁷ |
| Monomer #1 | Not Detected | Not Detected | 1.20 | 4.6 × 10 ⁷ |
| Monomer #2 | Not Detected | Not Detected | 1.27 | 1.1 × 10 ⁷ |

Analysis of the data indicated that a CD40-L monomer comprising solely the portion of the extracellular domain most homologous to TNF was capable of binding CD40, although with somewhat lower affinity than oligomeric CD40-L. An analysis of the ratio of binding in the second experiment demonstrated that there are twice as many CD40-L monomer units bound per CD40/Fc molecule as trimeric CD40-L, confirming that two monomers of CD40-L bind one CD40/Fc dimer and one trimeric CD40-L binds one CD40/Fc dimer.

EXAMPLE 23

This example demonstrates that CD40-L enhances the generation of cytotoxic T lymphocytes (CTL) in mixed lymphocyte cultures (MLC). A 4-hour ⁵¹Cr release assay was used to assess the cytolytic activity of human T cells essentially as described in Alderson et al., *J. Exp. Med.* 172:577 (1990). Briefly, freshly isolated peripheral blood mononuclear cells from one donor were cultured in MLC (mixed lymphocyte culture) with irradiated, allogeneic stimulating cells (target cells), either in the presence or absence of membrane-bound CD40-L. ⁵¹Cr-labeled target cells were prepared by incubating tumor cell lines, or three day PHA blasts from a second donor, with 100 μCi of ⁵¹Cr for one hour at 37°C.

Cell cultures to be assessed for cytolytic activity were washed twice in culture medium and serially diluted in 96-well V-bottom plates (Costar). ⁵¹Cr-labeled target cells (2 × 10³) were added to each well (total volume of 200 μl/well), and the plates were incubated for four hours at 37°C. After incubation, the plates were centrifuged at 150 g for five minutes, and harvested using a Skatron SCS harvesting system (Skatron, Sterling, VA). ⁵¹Cr content of the supernatants was determined using a Micromedic ME Plus gamma scintillation counter

(Micromedic, Huntsville, TN). Percent specific ^{51}Cr release was calculated according to the formula $100 \times (\text{experimental cpm} - \text{spontaneous cpm}) / (\text{maximum cpm} - \text{spontaneous cpm})$ where spontaneous cpm = cpm released in the absence of effector cells and maximum cpm = cpm released in the presence of 1N HCl. The results of this experiment indicated that membrane-bound CD40-L enhanced CTL generation. A polyclonal anti-IL-2 antiserum capable of neutralizing 10 ng/ml of IL-2 at a 1:500 dilution was used to demonstrate that CD40-L enhancement of CTL had both IL-2 dependent and IL-2 independent components.

Similar experiments were performed to analyze the phenotype of the responding cells. T cells were purified by rosetting with 2-aminoethylisothiuronium bromide hydrobromide-treated sheep red blood cells. CD4+ and CD8+ populations were further purified using immunomagnetic selection using a MACS (Milenyi Biotec, Sunnyvale, CA) according to the manufacturer's protocol. Whereas IL-2 enhanced CTL generation by PBMC, purified T cells and CD8+ T cells, CD40-L enhanced CTL generation by PBMC and purified T cells, but not by CD8+ T cells. Analysis of cytokine secretion using a CTLL assay for IL-2 or an ELISA for IFN- γ indicated that CD4+ cells costimulated with CD40-L produced 5 to 10-fold more IFN- γ and IL-2 than CD8+ cells. Moreover, CD40-L stimulated CD4+ cells were induced to become cytolytic in a lectin-mediated killing assay, whereas IL-2 costimulated both CD8+ and CD4+ cells to become cytolytic.

These data demonstrate that, in addition to accessory molecules expressed by antigen presenting cells, membrane proteins may be important in T-T cell interactions. The function of CD40-L may be to enhance the expansion of activated T cells within a proliferating T cell clone in a paracrine fashion.

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(ii) TITLE OF INVENTION: NOVEL CYTOKINE

(iii) NUMBER OF SEQUENCES: 23

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Apple Operating System 7.1
(D) SOFTWARE: Microsoft Word for Apple, version 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/969,703
(B) FILING DATE: October 23, 1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/805,723
(B) FILING DATE: December 5, 1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/783,707
(B) FILING DATE: October 25, 1991
(C) CLASSIFICATION:

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(C) REFERENCE/DOCKET NUMBER: 2802-C

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: MOUSE
15 (vii) IMMEDIATE SOURCE:
(B) CLONE: CD40-L
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..783
20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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| 30 | CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT | 96 |
| | Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu | |
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| 35 | ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA | 144 |
| | Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg | |
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| 40 | AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA | 192 |
| | Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val | |
| | 50 55 60 | |
| 45 | TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC | 240 |
| | Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser | |
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| 50 | TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG | 288 |
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| 55 | GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG | 336 |
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| 60 | CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA | 384 |
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| 65 | GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT | 432 |
| | Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr | |
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| 70 | TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG | 480 |
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| | 145 150 155 160 | |

| | | |
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| 10 | TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA | 624 |
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| 15 | AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG | 672 |
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| 20 | GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG | 720 |
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| | Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly | |
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| 25 | TTA CTC AAA CTC TGA | 783 |
| | Leu Leu Lys Leu | |
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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| Leu | Pro | Ala | Ser | Met | Lys | Ile | Phe | Met | Tyr | Leu | Leu | Thr | Val | Phe | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Thr | Gln | Met | Ile | Gly | Ser | Val | Leu | Phe | Ala | Val | Tyr | Leu | His | Arg | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |
| Arg | Leu | Asp | Lys | Val | Glu | Glu | Glu | Val | Asn | Leu | His | Glu | Asp | Phe | Val | |
| | | 50 | | | | 55 | | | | | 60 | | | | | |
| Phe | Ile | Lys | Lys | Leu | Lys | Arg | Cys | Asn | Lys | Gly | Glu | Gly | Ser | Leu | Ser | |
| | | 65 | | | 70 | | | | | 75 | | | | 80 | | |
| Leu | Leu | Asn | Cys | Glu | Glu | Met | Arg | Arg | Gln | Phe | Glu | Asp | Leu | Val | Lys | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |
| Asp | Ile | Thr | Leu | Asn | Lys | Glu | Glu | Lys | Lys | Glu | Asn | Ser | Phe | Glu | Met | |
| | | 100 | | | | | 105 | | | | | 110 | | | | |
| Gln | Arg | Gly | Asp | Glu | Asp | Pro | Gln | Ile | Ala | Ala | His | Val | Val | Ser | Glu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |

Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
130 135 140

5 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
165 170 175

10 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
180 185 190

15 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
195 200 205

Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
210 215 220

20 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
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25 Leu Leu Lys Leu
260

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA 60

55 AAATCACAC ATGCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC 120

TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCC GACCCCTGAG GTCACATGCG 180

TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG 240

60 TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG 300

TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA 360

5 AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAAA GCCAAAGGGC 420
 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCCG GGATGAGCTG ACCAAGAACC 480
 AGGTGAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG 540
 AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG 600
 10 GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG 660
 TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT 720
 CCCTGTCTCC GGGTAAATGA 740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGAACCACC CACTGCATGC AGAGAAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT 60
 TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC 120
 TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC 180
 45 ACAAATACTG CGACCCCAAC CTAGGGCTTC GGTCCAGCA GAAGGGCACC TCAGAAACAG 240
 ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG 300
 TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGTCAAGCA GATTGCTACA GGGGTTTCTG 360
 50 ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA 420
 AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA 480
 55 ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA 519

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGTCGACCA CCATGGTTCG TCTGCC

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 3' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGTCGACGT CTAGAGCCGA TCCTGGGG

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: internal

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PENTAPEPTIDE

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PCR PRIMER

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HUMAN IGG1/FC 5' PRIMER

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAAC CAC

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGGAGA CAGGGAGA

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCCACCTTC TCTGCCAGAA GATACCATTT CAACTTTAAC ACAGC ATG ATC GAA

54

Met Ile Glu

1

ACA TAC AAC CAA ACT TCT CCC CGA TCT GCG GCC ACT GGA CTG CCC ATC
Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly Leu Pro Ile

102

5

10

15

AGC ATG AAA ATT TTT ATG TAT TTA CTT ACT GTT TTT CTT ATC ACC CAG
Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln

150

20

25

30

35

ATG ATT GGG TCA GCA CTT TTT GCT GTG TAT CTT CAT AGA AGG TTG GAC
Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp

198

40

45

50

AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA
Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys

246

55

60

65

ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC
Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn

294

70

75

80

TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG
Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met

342

| | 85 | 90 | 95 | |
|----|---|----|----|-----|
| 5 | TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys 100 105 110 115 | | | 390 |
| 10 | GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser 120 125 130 | | | 438 |
| 15 | AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr 135 140 145 | | | 486 |
| 20 | ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val 150 155 160 | | | 534 |
| 25 | AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser 165 170 175 | | | 582 |
| 30 | AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu 180 185 190 195 | | | 630 |
| 35 | AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr 200 205 210 | | | 678 |
| 40 | CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly 215 220 225 | | | 726 |
| 45 | GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp 230 235 240 | | | 774 |
| 50 | CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu 245 250 255 | | | 822 |
| 55 | AAA CTC TGAACAGTGT CA Lys Leu 260 | | | 840 |

(2) INFORMATION FOR SEQ ID NO:12:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|----|--|
| 60 | Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly 1 5 10 15 |
| | Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu 20 25 30 |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Ile | Thr | Gln | Met | Ile | Gly | Ser | Ala | Leu | Phe | Ala | Val | Tyr | Leu | His | Arg | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 5 | Arg | Leu | Asp | Lys | Ile | Glu | Asp | Glu | Arg | Asn | Leu | His | Glu | Asp | Phe | Val | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| | Phe | Met | Lys | Thr | Ile | Gln | Arg | Cys | Asn | Thr | Gly | Glu | Arg | Ser | Leu | Ser | |
| | | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| 10 | Leu | Leu | Asn | Cys | Glu | Glu | Ile | Lys | Ser | Gln | Phe | Glu | Gly | Phe | Val | Lys | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| | Asp | Ile | Met | Leu | Asn | Lys | Glu | Glu | Thr | Lys | Lys | Glu | Asn | Ser | Phe | Glu | |
| 15 | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Met | Gln | Lys | Gly | Asp | Gln | Asn | Pro | Gln | Ile | Ala | Ala | His | Val | Ile | Ser | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 20 | Glu | Ala | Ser | Ser | Lys | Thr | Thr | Ser | Val | Leu | Gln | Trp | Ala | Glu | Lys | Gly | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Tyr | Tyr | Thr | Met | Ser | Asn | Asn | Leu | Val | Thr | Leu | Glu | Asn | Gly | Lys | Gln | |
| 25 | | | | | | 150 | | | | | 155 | | | | | 160 | |
| | Leu | Thr | Val | Lys | Arg | Gln | Gly | Leu | Tyr | Tyr | Ile | Tyr | Ala | Gln | Val | Thr | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| | Phe | Cys | Ser | Asn | Arg | Glu | Ala | Ser | Ser | Gln | Ala | Pro | Phe | Ile | Ala | Ser | |
| 30 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Leu | Cys | Leu | Lys | Ser | Pro | Gly | Arg | Phe | Glu | Arg | Ile | Leu | Leu | Arg | Ala | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 35 | Ala | Asn | Thr | His | Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Leu | Gly | Gly | Val | Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | |
| 40 | | 225 | | | | 230 | | | | 235 | | | | | | 240 | |
| | Val | Thr | Asp | Pro | Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 45 | Gly | Leu | Leu | Lys | Leu | | | | | | | | | | | | |
| | | | | 260 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:13:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGCTGGCCGA GGGTCAGGCG GAGGTGGGTC CGGAGGCGGG GGTTCAGTT CTGACAAGAT 60
5 AGAAGATGAA AGG 73

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCGCTCAG AGTTTGAGTA A 21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Human CD40-L/FC2 (soluble CD40-L)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..1422

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 79..1422

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 4..78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAT ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG 48
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-25 -20 -15

| | | |
|----|---|-----|
| | ATC CTT GTT CTG CTG CCT GTC ACT AGC TCT GAC TAC AAA GAT GAC GAT | 96 |
| | Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp | |
| | -10 -5 1 5 | |
| 5 | GAT AAA AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA | 144 |
| | Asp Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala | |
| | 10 15 20 | |
| 10 | CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC | 192 |
| | Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro | |
| | 25 30 35 | |
| 15 | AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG | 240 |
| | Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val | |
| | 40 45 50 | |
| 20 | GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG | 288 |
| | Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val | |
| | 55 60 65 70 | |
| 25 | GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG | 336 |
| | Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln | |
| | 75 80 85 | |
| 30 | TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG | 384 |
| | Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln | |
| | 90 95 100 | |
| 35 | GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC | 432 |
| | Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala | |
| | 105 110 115 | |
| 40 | CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC | 480 |
| | Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro | |
| | 120 125 130 | |
| 45 | CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC | 528 |
| | Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr | |
| | 135 140 145 150 | |
| 50 | AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC | 576 |
| | Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser | |
| | 155 160 165 | |
| 55 | GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC | 624 |
| | Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr | |
| | 170 175 180 | |
| 60 | AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC | 672 |
| | Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr | |
| | 185 190 195 | |
| 65 | AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC | 720 |
| | Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe | |
| | 200 205 210 | |
| 70 | TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC | 768 |
| | Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser | |
| | 215 220 225 230 | |
| 75 | GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT | 816 |
| | Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu | |
| | 235 240 245 | |

| | | |
|----|---|------|
| | CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA | 864 |
| | His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly | |
| | 250 255 260 | |
| 5 | GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT | 912 |
| | Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe | |
| | 265 270 275 | |
| 10 | GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA | 960 |
| | Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys | |
| | 280 285 290 | |
| 15 | GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG | 1008 |
| | Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala | |
| | 295 300 305 310 | |
| 20 | GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG | 1056 |
| | Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln | |
| | 315 320 325 | |
| | TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG | 1104 |
| | Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu | |
| | 330 335 340 | |
| 25 | GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC | 1152 |
| | Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile | |
| | 345 350 355 | |
| 30 | TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT | 1200 |
| | Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala | |
| | 360 365 370 | |
| 35 | CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA | 1248 |
| | Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg | |
| | 375 380 385 390 | |
| 40 | ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG | 1296 |
| | Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly | |
| | 395 400 405 | |
| 45 | CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT | 1344 |
| | Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala | |
| | 410 415 420 | |
| 50 | TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT | 1392 |
| | Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr | |
| | 425 430 435 | |
| 55 | GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA | 1425 |
| | Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu | |
| | 440 445 | |

55 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-25 -20 -15 -10

10 Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp
-5 1 5

15 Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
10 15 20

20 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
25 30 35

25 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
40 45 50 55

30 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
60 65 70

35 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
75 80 85

40 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
90 95 100

45 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
105 110 115

50 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
120 125 130 135

55 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
140 145 150

60 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
155 160 165

65 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
170 175 180

70 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
185 190 195

75 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
200 205 210 215

80 Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
220 225 230

85 Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu His
235 240 245

90 Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu
250 255 260

95 Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu
265 270 275

100 Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu
280 285 290 295

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala

300

305

310

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
315 320 325

Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
330 335 340

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
345 350 355

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
360 365 370 375

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
380 385 390

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
395 400 405

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
410 415 420

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
425 430 435

Phe Thr Ser Phe Gly Leu Leu Lys Leu
440 445

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT 21

10 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA 35

30 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..142

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 65..886

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 143..886

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC 60

60 CACC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG 109
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-26 -25 -20 -15

ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG AAA CAG ATA 157

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ile | Leu | Val | Leu | Leu | Pro | Val | Thr | Ser | Ser | Asp | Arg | Met | Lys | Gln | Ile | |
| | -10 | | | | | | -5 | | | | | 1 | | | | 5 | |
| 5 | GAG | GAT | AAG | ATC | GAA | GAG | ATC | CTA | AGT | AAG | ATT | TAT | CAT | ATA | GAG | AAT | 205 |
| | Glu | Asp | Lys | Ile | Glu | Glu | Ile | Leu | Ser | Lys | Ile | Tyr | His | Ile | Glu | Asn | |
| | | | | | 10 | | | | | 15 | | | | | 20 | | |
| 10 | GAA | ATC | GCC | CGT | ATC | AAA | AAG | CTG | ATT | GGC | GAG | CGG | ACT | AGT | TCT | GAC | 253 |
| | Glu | Ile | Ala | Arg | Ile | Lys | Lys | Leu | Ile | Gly | Glu | Arg | Thr | Ser | Ser | Asp | |
| | | | | 25 | | | | | 30 | | | | | 35 | | | |
| 15 | AAG | ATA | GAA | GAT | GAA | AGG | AAT | CTT | CAT | GAA | GAT | TTT | GTA | TTC | ATG | AAA | 301 |
| | Lys | Ile | Glu | Asp | Glu | Arg | Asn | Leu | His | Glu | Asp | Phe | Val | Phe | Met | Lys | |
| | | | 40 | | | | | 45 | | | | | 50 | | | | |
| 20 | ACG | ATA | CAG | AGA | TGC | AAC | ACA | GGA | GAA | AGA | TCC | TTA | TCC | TTA | CTG | AAC | 349 |
| | Thr | Ile | Gln | Arg | Cys | Asn | Thr | Gly | Glu | Arg | Ser | Leu | Ser | Leu | Leu | Asn | |
| | | 55 | | | | | 60 | | | | | 65 | | | | | |
| 25 | TGT | GAG | GAG | ATT | AAA | AGC | CAG | TTT | GAA | GGC | TTT | GTG | AAG | GAT | ATA | ATG | 397 |
| | Cys | Glu | Glu | Ile | Lys | Ser | Gln | Phe | Glu | Gly | Phe | Val | Lys | Asp | Ile | Met | |
| | | 70 | | | | 75 | | | | | 80 | | | | | 85 | |
| 30 | TTA | AAC | AAA | GAG | GAG | ACG | AAG | AAA | GAA | AAC | AGC | TTT | GAA | ATG | CAA | AAA | 445 |
| | Leu | Asn | Lys | Glu | Glu | Thr | Lys | Lys | Glu | Asn | Ser | Phe | Glu | Met | Gln | Lys | |
| | | | | | 90 | | | | | 95 | | | | | 100 | | |
| 35 | GGT | GAT | CAG | AAT | CCT | CAA | ATT | GCG | GCA | CAT | GTC | ATA | AGT | GAG | GCC | AGC | 493 |
| | Gly | Asp | Gln | Asn | Pro | Gln | Ile | Ala | Ala | His | Val | Ile | Ser | Glu | Ala | Ser | |
| | | | | 105 | | | | | 110 | | | | | 115 | | | |
| 40 | AGT | AAA | ACA | ACA | TCT | GTG | TTA | CAG | TGG | GCT | GAA | AAA | GGA | TAC | TAC | ACC | 541 |
| | Ser | Lys | Thr | Thr | Ser | Val | Leu | Gln | Trp | Ala | Glu | Lys | Gly | Tyr | Tyr | Thr | |
| | | | 120 | | | | | 125 | | | | | 130 | | | | |
| 45 | ATG | AGC | AAC | AAC | TTG | GTA | ACC | CTG | GAA | AAT | GGG | AAA | CAG | CTG | ACC | GTT | 589 |
| | Met | Ser | Asn | Asn | Leu | Val | Thr | Leu | Glu | Asn | Gly | Lys | Gln | Leu | Thr | Val | |
| | | 135 | | | | | 140 | | | | | 145 | | | | | |
| 50 | AAA | AGA | CAA | GGA | CTC | TAT | TAT | ATC | TAT | GCC | CAA | GTC | ACC | TTC | TGT | TCC | 637 |
| | Lys | Arg | Gln | Gly | Leu | Tyr | Tyr | Ile | Tyr | Ala | Gln | Val | Thr | Phe | Cys | Ser | |
| | | 150 | | | | 155 | | | | | 160 | | | | | 165 | |
| 55 | AAT | CGG | GAA | GCT | TCG | AGT | CAA | GCT | CCA | TTT | ATA | GCC | AGC | CTC | TGC | CTA | 685 |
| | Asn | Arg | Glu | Ala | Ser | Ser | Gln | Ala | Pro | Phe | Ile | Ala | Ser | Leu | Cys | Leu | |
| | | | | 170 | | | | | | 175 | | | | | 180 | | |
| 60 | AAG | TCC | CCC | GGT | AGA | TTC | GAG | AGA | ATC | TTA | CTC | AGA | GCT | GCA | AAT | ACC | 733 |
| | Lys | Ser | Pro | Gly | Arg | Phe | Glu | Arg | Ile | Leu | Leu | Arg | Ala | Ala | Asn | Thr | |
| | | | 185 | | | | | 190 | | | | | 195 | | | | |
| 65 | CAC | AGT | TCC | GCC | AAA | CCT | TGC | GGG | CAA | CAA | TCC | ATT | CAC | TTG | GGA | GGA | 781 |
| | His | Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | Leu | Gly | Gly | |
| | | | 200 | | | | | 205 | | | | | 210 | | | | |
| 70 | GTA | TTT | GAA | TTG | CAA | CCA | GGT | GCT | TCG | GTG | TTT | GTC | AAT | GTG | ACT | GAT | 829 |
| | Val | Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | Val | Thr | Asp | |
| | | 215 | | | | | 220 | | | | | 225 | | | | | |
| 75 | CCA | AGC | CAA | GTG | AGC | CAT | GGC | ACT | GGC | TTC | ACG | TCC | TTT | GGC | TTA | CTC | 877 |
| | Pro | Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | Gly | Leu | Leu | |
| | | 230 | | | | 235 | | | | | 240 | | | | | 245 | |

929

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Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
235 240 245

5 Leu

(2) INFORMATION FOR SEQ ID NO:22:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 878 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(B) CLONE: Murine CD40-L trimer
- 20 (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 15..92
- 25 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15..857
- 30 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35 CTCGAGGTAC CGCC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT 50
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile
-26 -25 -20 -15

40 CCT CCA CTG ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG 98
Pro Pro Leu Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met
-10 -5 1

45 AAA CAG ATA GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT 146
Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
5 10 15

50 ATA GAG AAT GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT 194
Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
20 25 30

AGT TCT GAC TAC AAA GAT GAC GAT GAT AAA GAT AAG GTC GAA GAG GAA 242
Ser Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu
35 40 45 50

55 GTA AAC CTT CAT GAA GAT TTT GTA TTC ATA AAA AAG CTA AAG AGA TGC 290
Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys
55 60 65

60 AAC AAA GGA GAA GGA TCT TTA TCC TTG CTG AAC TGT GAG GAG ATG AGA 338
Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg
70 75 80

| | | |
|----|---|-----|
| | AGG CAA TTT GAA GAC CTT GTC AAG GAT ATA ACG TTA AAC AAA GAA GAG | 386 |
| | Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu | |
| | 85 90 95 | |
| 5 | AAA AAA GAA AAC AGC TTT GAA ATG CAA AGA GGT GAT GAG GAT CCT CAA | 434 |
| | Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln | |
| | 100 105 110 | |
| 10 | ATT GCA GCA CAC GTT GTA AGC GAA GCC AAC AGT AAT GCA GCA TCC GTT | 482 |
| | Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val | |
| | 115 120 125 130 | |
| 15 | CTA CAG TGG GCC AAG AAA GGA TAT TAT ACC ATG AAA AGC AAC TTG GTA | 530 |
| | Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val | |
| | 135 140 145 | |
| 20 | ATG CTT GAA AAT GGG AAA CAG CTG ACG GTT AAA AGA GAA GGA CTC TAT | 578 |
| | Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr | |
| | 150 155 160 | |
| 25 | TAT GTC TAC ACT CAA GTC ACC TTC TGC TCT AAT CGG GAG CCT TCG AGT | 626 |
| | Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser | |
| | 165 170 175 | |
| 30 | CAA CGC CCA TTC ATC GTC GGC CTC TGG CTG AAG CCC AGC AGT GGA TCT | 674 |
| | Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser | |
| | 180 185 190 | |
| 35 | GAG AGA ATC TTA CTC AAG GCG GCA AAT ACC CAC AGT TCC TCC CAG CTT | 722 |
| | Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu | |
| | 195 200 205 210 | |
| 40 | TGC GAG CAG CAG TCT GTT CAC TTG GGC GGA GTG TTT GAA TTA CAA GCT | 770 |
| | Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala | |
| | 215 220 225 | |
| 45 | GGT GCT TCT GTG TTT GTC AAC GTG ACT GAA GCA AGC CAA GTG ATC CAC | 818 |
| | Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His | |
| | 230 235 240 | |
| 50 | AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC | 864 |
| | Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu | |
| | 245 250 255 | |
| 55 | CGCTACAGAT CTAC | 878 |

(2) INFORMATION FOR SEQ ID NO:23:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

60 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
 -26 -25 -20 -15

Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
 -10 -5 1 5

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Asp | Lys | Ile | Glu | Glu | Ile | Leu | Ser | Lys | Ile | Tyr | His | Ile | Glu | Asn | Glu | |
| | | | | 10 | | | | | 15 | | | | | 20 | | | |
| 5 | Ile | Ala | Arg | Ile | Lys | Lys | Leu | Ile | Gly | Glu | Arg | Thr | Ser | Ser | Asp | Tyr | |
| | | | 25 | | | | | 30 | | | | | 35 | | | | |
| | Lys | Asp | Asp | Asp | Asp | Lys | Asp | Lys | Val | Glu | Glu | Glu | Val | Asn | Leu | His | |
| | | 40 | | | | | 45 | | | | | 50 | | | | | |
| 10 | Glu | Asp | Phe | Val | Phe | Ile | Lys | Lys | Leu | Lys | Arg | Cys | Asn | Lys | Gly | Glu | |
| | | 55 | | | | 60 | | | | | 65 | | | | | 70 | |
| | Gly | Ser | Leu | Ser | Leu | Leu | Asn | Cys | Glu | Glu | Met | Arg | Arg | Gln | Phe | Glu | |
| 15 | | | | | 75 | | | | | 80 | | | | | 85 | | |
| | Asp | Leu | Val | Lys | Asp | Ile | Thr | Leu | Asn | Lys | Glu | Glu | Lys | Lys | Glu | Asn | |
| | | | | 90 | | | | | 95 | | | | | 100 | | | |
| 20 | Ser | Phe | Glu | Met | Gln | Arg | Gly | Asp | Glu | Asp | Pro | Gln | Ile | Ala | Ala | His | |
| | | | 105 | | | | | 110 | | | | | 115 | | | | |
| | Val | Val | Ser | Glu | Ala | Asn | Ser | Asn | Ala | Ala | Ser | Val | Leu | Gln | Trp | Ala | |
| | | 120 | | | | | 125 | | | | | 130 | | | | | |
| 25 | Lys | Lys | Gly | Tyr | Tyr | Thr | Met | Lys | Ser | Asn | Leu | Val | Met | Leu | Glu | Asn | |
| | | 135 | | | | 140 | | | | | 145 | | | | | 150 | |
| | Gly | Lys | Gln | Leu | Thr | Val | Lys | Arg | Glu | Gly | Leu | Tyr | Tyr | Val | Tyr | Thr | |
| 30 | | | | | 155 | | | | | 160 | | | | | 165 | | |
| | Gln | Val | Thr | Phe | Cys | Ser | Asn | Arg | Glu | Pro | Ser | Ser | Gln | Arg | Pro | Phe | |
| | | | | 170 | | | | | 175 | | | | | 180 | | | |
| 35 | Ile | Val | Gly | Leu | Trp | Leu | Lys | Pro | Ser | Ser | Gly | Ser | Glu | Arg | Ile | Leu | |
| | | | 185 | | | | 190 | | | | | | 195 | | | | |
| | Leu | Lys | Ala | Ala | Asn | Thr | His | Ser | Ser | Ser | Gln | Leu | Cys | Glu | Gln | Gln | |
| | | 200 | | | | | 205 | | | | | 210 | | | | | |
| 40 | Ser | Val | His | Leu | Gly | Gly | Val | Phe | Glu | Leu | Gln | Ala | Gly | Ala | Ser | Val | |
| | | 215 | | | | 220 | | | | | 225 | | | | | 230 | |
| | Phe | Val | Asn | Val | Thr | Glu | Ala | Ser | Gln | Val | Ile | His | Arg | Val | Gly | Phe | |
| 45 | | | | | 235 | | | | | 240 | | | | | 245 | | |
| | Ser | Ser | Phe | Gly | Leu | Leu | Lys | Leu | | | | | | | | | |
| | | | | 250 | | | | | | | | | | | | | |

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CLAIMS

What is claimed is:

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1. An isolated DNA encoding a CD40-L polypeptide, wherein the DNA is selected from the group consisting of:

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(a) DNA comprising nucleotides 46 through 828, 196 through 828, 193 through 762, 403 through 828, or 403 through 762 of SEQ ID NO:11 and their complementary strands;

(b) DNA which hybridizes to one of the DNA molecules of (a) under stringent conditions (hybridization in 6 X SSC at 63°C overnight; washing in 3 X SSC at 55°C), and which encodes a polypeptide that binds to CD40; and

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(c) DNA which, due to degeneracy of the genetic code, encodes a polypeptide encoded by any of the foregoing DNA sequences, wherein the polypeptide binds to CD40.

2. The isolated DNA according to claim 1 encoding a soluble CD40-L polypeptide.

3. The isolated DNA according to claim 2 which further comprises a DNA encoding a leucine zipper peptide.

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4. The isolated DNA according to claim 3 wherein the leucine zipper peptide is a peptide having an amino acid sequence represented by SEQ ID NO:17.

5. The isolated DNA according to claim 4 which encodes a peptide having an amino acid sequence represented by SEQ ID NO:21.

6. The isolated DNA according to claim 2 which further comprises a DNA encoding an immunoglobulin Fc region.

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7. The isolated DNA sequence according to claim 6 wherein the Fc region is a human IgG₁ Fc region.

8. The isolated DNA according to claim 7 which encodes a peptide having an amino acid sequence as represented by amino acid 1 through 448 of SEQ ID NO:16.

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9. A recombinant expression vector comprising a DNA sequence according to claim 1.

10. A recombinant expression vector comprising a DNA sequence according to claim 2.

11. A recombinant expression vector comprising a DNA sequence according to claim 5.

12. A host cell transformed or transfected with an expression vector according to claim 9.
13. A host cell transformed or transfected with an expression vector according to claim 10.
14. A host cell transformed or transfected with an expression vector according to claim 11.
15. A process for preparing a CD40-L polypeptide, comprising culturing a host cell according to claim 13 under conditions promoting expression and recovering CD40-L polypeptide from the culture.
16. A process for preparing a CD40-L polypeptide, comprising culturing a host cell according to claim 14 under conditions promoting expression and recovering CD40-L polypeptide from the culture.
17. A purified CD40-L polypeptide that binds CD40 comprising a sequence of amino acids encoded by a nucleotide sequence according to claim 1.
18. The purified CD40-L polypeptide according to claim 17, wherein the CD40-L is a soluble CD40-L.
19. The soluble CD40-L according to claim 18, wherein the soluble CD40-L comprises amino acids 51 through 261 of SEQ ID NO:11.
20. The soluble CD40-L according to claim 19 wherein the CD40-L is an oligomer comprising two or more CD40-L extracellular regions.
21. The soluble CD40-L according to claim 20 having an amino acid sequence represented by SEQ ID NO:21
22. A method of treating allergy, an allergic reaction, lupus, rheumatoid arthritis or graft versus host disease comprising administering an effective amount of a CD40 antagonist selected from the group consisting of a soluble CD40 protein, a CD40 fusion protein, a soluble monomeric CD40-L polypeptide, and combinations thereof.
23. A method of augmenting a vaccine response with an adjuvant, wherein the adjuvant is selected from the group consisting of a membrane-bound CD40-L polypeptide, oligomeric soluble CD40-L polypeptides, and combinations thereof.

24. A method for stimulating hybridoma cells to increase monoclonal antibody secretion, comprising administering an effective amount of a CD40 agonist selected from the group consisting of CD40-L, membrane-bound CD40-L and oligomeric CD40-L.

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25. An antibody immunoreactive with CD40-L or a CD40-L immunogen.

26. An antibody according to claim 25 which is a monoclonal antibody.

10 27. An isolated oligonucleotide comprising an oligonucleotide of at least about 12 nucleotides of SEQ ID NO:11 or its complement, which hybridizes to a DNA according to claim 1 under moderately stringent conditions (50°C, 5 X SSC).

ABSTRACT OF THE DISCLOSURE

- 5 There is disclosed a polypeptide (CD40-L) and DNA sequences, vectors and transformed host cells useful in providing CD40-L polypeptides. More particularly, this invention provides isolated human and murine CD40-L polypeptides that bind to the extracellular binding region of a CD40 receptor.

FIG. 1

| | | |
|-----|--|-----|
| 1 | CTTTCAAGTATGATAGAAAACATACAGCCAAACCTTCCCCCAGATCCGTGGCAACTGGACTTCCAGCG | 69 |
| 1 | MetIleGluThrTyrSerGlnProSerProArgSerValAlaThrGlyLeuProAla | 19 |
| 70 | AGCATGAAGATTTTATGTATTACTTACTGTTTTTCCCTTATCACCACCAATGATTGGATCTGTGCTTTTT | 138 |
| 20 | SerMetLysIlePheMetTyrLeuLeuThrValPheLeuIleThrGlnMetIleGlySerValLeuPhe | 42 |
| 139 | GCTGTGTATCTTCATAGAAAGATTGGATAAGGTCGAAGAGGAAGTAAACCTTTCATGAAGATTTTGTATTC | 207 |
| 43 | AlaValTyrLeuHisArgArgLeuAspLysValGluGluValAlaAsnLeuHisGluAspPheValPhe | 65 |
| 208 | ATAAAAAAGCTAAAGAGATGCAACAAAGGAGAGGATCTTTATCTTGTGCTGAACCTGTGAGGAGATGAGA | 276 |
| 66 | IleLysLysLeuLysArgCysAsnLysGlyGluGlySerLeuSerLeuLeuAsnCysGluGluMetArg | 88 |
| 277 | AGGCAATTTGAAGACCTTGTCAAGGATATAACGTTAAACAAAGAGAGAAAAAAGAAACAGCTTTTGAA | 345 |
| 89 | ArgGlnPheGluAspLeuValLysAspIleThrLeuAsnLysGluGluLysLysGluAsnSerPheGlu | 111 |
| 346 | ATGCAAAAGAGGTGATGAGGATCCTCAAATTGCAGCACACGTTGTAAAGCGAAGCCAAACAGTAATGCAGCA | 414 |
| 112 | MetGlnArgGlyAspGluAspProGlnIleAlaAlaHisValSerGluAlaAsnSerAsnAlaAla | 134 |
| 415 | TCCGTTCTACAGTGGGCCAAGAAAGGATATTATACCATGAAAAGCAACTTGGTAATGCTTGAAAAATGGG | 483 |
| 135 | SerValLeuGlnTrpAlaLysLysGlyTyrTyrThrMetLysSerAsnLeuValMetLeuGluAsnGly | 157 |
| 484 | AAACAGCTGACGGTTAAAAGAGAAAGGACTCTATTATGTCTACACTCAAGTCACCTTCTGTCTAATCAGG | 552 |
| 158 | LysGlnLeuThrValLysArgGluGlyLeuTyrTyrValTyrThrGlnValThrPheCysSerAsnArg | 180 |
| 553 | GAGCCTTCGAGTCAACGCCCATTCATCGTCGGCCTCTGGCTGAAGCCCAGCAGTGGATCTGAGAGAATC | 621 |
| 181 | GluProSerSerGlnArgProPheIleValGlyLeuTrpLeuLysProSerSerGlySerGluArgIle | 203 |
| 622 | TTACTCAAGGCGGCAAAATACCCACAGTTCTCCACGCTTTGCGAGCAGCAGTCTGTTCACTTGGGCGGA | 690 |
| 204 | LeuLeuLysAlaAlaAsnThrHisSerSerSerGlnLeuCysGluGlnGlnSerValHisLeuGlyGly | 226 |

FIG. 1, continued

| | | |
|------|--|------|
| 691 | GTGTTTGAATTACAAGCTGGTGTCTCTGTGTTTGTCAACGTGACTGAAGCAAGCCAAAGTGATCCACAGA | 759 |
| 227 | ValPheGluLeuGlnAlaGlyAlaSerValPheValAsnValThrGluAlaSerGlnValIleHisArg | 249 |
| 760 | GTTGGCTTCTCATCTTTTGGCTTACTCAAACCTCTGAACAGTGGCTGCCCTAGGCTGCAGCAGGGCTGA | 828 |
| 250 | ValGlyPheSerSerPheGlyLeuLeuLysLeu | 260 |
| 829 | TGCTGGCAGTCTCCCCCTATACACCAAGTCAGTTAGGCCCTCCCCCTGTGTGAACTGCCTATTATAACC | 897 |
| 898 | CTAGGATCCTCCTCATGGAGAACTATTTATTATGTACCCCAAGGCACATAGAGCTGGAATAAGAGAAT | 966 |
| 967 | TACAGGGCAGGCAGAAAATCCCCAAGGGACCCCTGCTCCCTTAAGAACTTACAATCTGAAACAGCAACCCAC | 1035 |
| 1036 | TGATTCAGACAACCAAGAAAGACAAAGCCATAATACACAGATGACAGAGCTCTGATGAAACAAACAGATA | 1104 |
| 1105 | ACTAATGAGCACAGTTTTTGTGTTTATGGGTGTGTCGTTCAATGGACAGTGTACTIONTACTTACCAGGG | 1173 |
| 1174 | AAGATGCAGAAGGGCAACTGTGAGCCCTCAGCTCACAAATCTGTTATGGTTGACCTGGGCTCCCTGCGGCC | 1242 |
| 1243 | CTAGTAGG | 1250 |

FIG. 2

| | | |
|-----|--|-----|
| 1 | TGCCACCTTCTCTGCCAGAAGATACCATTTCAACTTTAACACAGCATGATCGAAAACATACAACCAAACT | 69 |
| 1 | MetIleGluThrTyrAsnGlnThr | 8 |
| 70 | TCTCCCCGATCTGCGGCCACTGGACTGCCCATCAGCATGAAAATTTTATGTATTACTTACTGTTTTT | 138 |
| 9 | SerProArgSerAlaAlaThrGlyLeuProIleSerMetLysIlePheMetTyrLeuLeuThrValPhe | 31 |
| 139 | CTTATCACCCAGATGATTGGGTGAGCAGCCTTTTGTCTGTGTATCTTCATAGAGGTTGGACAAGATAGAA | 207 |
| 32 | LeuIleThrGlnMetIleGlySerAlaLeuPheAlaValTyrLeuHisArgArgLeuAspLysIleGlu | 54 |
| 208 | GATGAAAGGAATCTTCATGAAGATTTTGTATTTCATGAAAACGATACAGAGATGCAACACAGGAGAAAAGA | 276 |
| 55 | AspGluArgAsnLeuHisGluAspPheValPheMetLysThrIleGlnArgCysAsnThrGlyGluArg | 77 |
| 277 | TCCTTATCCTTACTGAACTGTGAGGAGATTAAAAGCCAGTTTGAAGGCTTTGTGAAGGATATAATGTTA | 345 |
| 78 | SerLeuSerLeuLeuAsnCysGluGluIleLysSerGlnPheGluGlyPheValLysAspIleMetLeu | 100 |
| 346 | AACAAAGAGAGACGAAGAAAAGAAAACAGCTTTTGAAATGC AAAAAGGTGATCAGAATCCTCAAAATTGCG | 414 |
| 101 | AsnLysGluGluThrLysLysGluAsnSerPheGluMetGlnLysGlyAspGlnAsnProGlnIleAla | 123 |
| 415 | GCACATGTCATAAGTGAGGCCAGCAGTAAACAACATCTGTGTTACAGTGGGCTGAAAAAGGATAC | 483 |
| 124 | AlaHisValIleSerGluAlaSerSerLysThrThrSerValLeuGlnTrpAlaGluLysGlyTyrTyr | 146 |
| 484 | ACCATGAGCAACAACCTTGGTAACCTGCAAAATGGGAAACAGCTGACCGTTAAAAGACAAGGACTCTAT | 552 |
| 147 | ThrMetSerAsnAsnLeuValThrLeuGluAsnGlyLysGlnLeuThrValLysArgGlnGlyLeuTyr | 169 |
| 553 | TATATCTATGCCCCAAGTCACCTTCTGTTCCTCAATCGGGAAGCTTCGAGTCAAGCTCCATTATAGCCAGC | 621 |
| 170 | TyrIleTyrAlaGlnValThrPheCysSerAsnArgGluAlaSerSerGlnAlaProPheIleAlaSer | 192 |
| 622 | CTCTGCCTAAAGTCCCCGGTAGATTTCGAGAGAATCTTACTCAGAGCTGCAAAATACCCACAGTTCCGCC | 690 |
| 193 | LeuCysLeuLysSerProGlyArgPheGluArgIleLeuLeuArgAlaAlaAsnThrHisSerSerAla | 215 |

FIG. 2, continued

| | | |
|-----|---|-----|
| 691 | AAACCTTGCGGGCAACAATCCATTCACTTGGGAGGAGTATTGAAATTGCAACCAGGTGCTTCGGTGT | 759 |
| 216 | LysProCysGlyGlnGlnSerIleHisLeuGlyGlyValPheGluLeuGlnProGlyAlaSerValPhe | 238 |
| 760 | GTCAATGTGACTGATCCAAGCCAAGTGAGCCATGGCACTGGCTTCACGTCCTTTGGCTTACTCAA | 828 |
| 239 | ValAsnValThrAspProSerGlnValSerHisGlyThrGlyPheThrSerPheGlyLeuLeuLysLeu | 261 |
| 829 | TGAACAGTGTCAACCTTGCAGGCTGTGTGGAGCTGACGCTGGGAGTCTTCATAATACAGCACAGCGG | 897 |
| 898 | AAGCCACCCCCCTGTTAACTGCCCTATTATTAACCCTAGGATCCTCCTTATGGAGAACTATTAT | 961 |

FIG. 4A

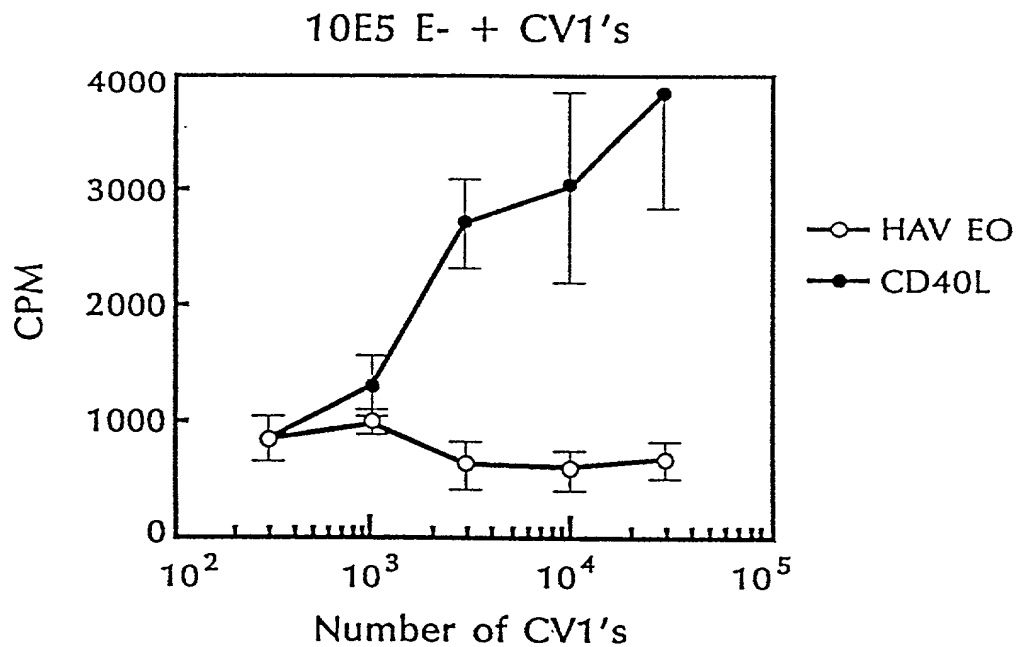


FIG. 4B

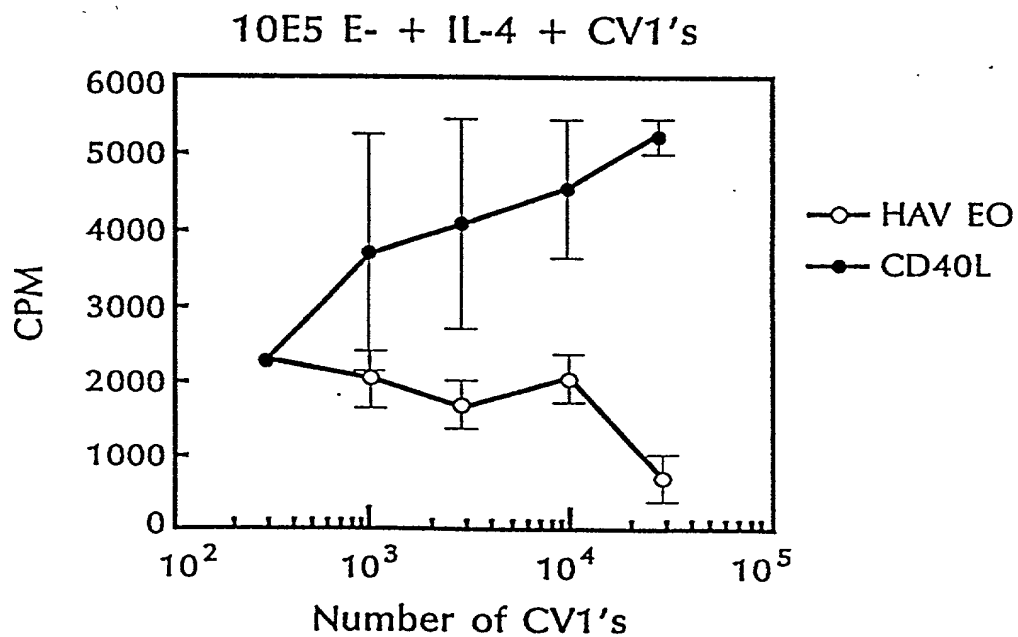


FIG. 5

PB E + IL-4 + CV1 d7 Proliferation

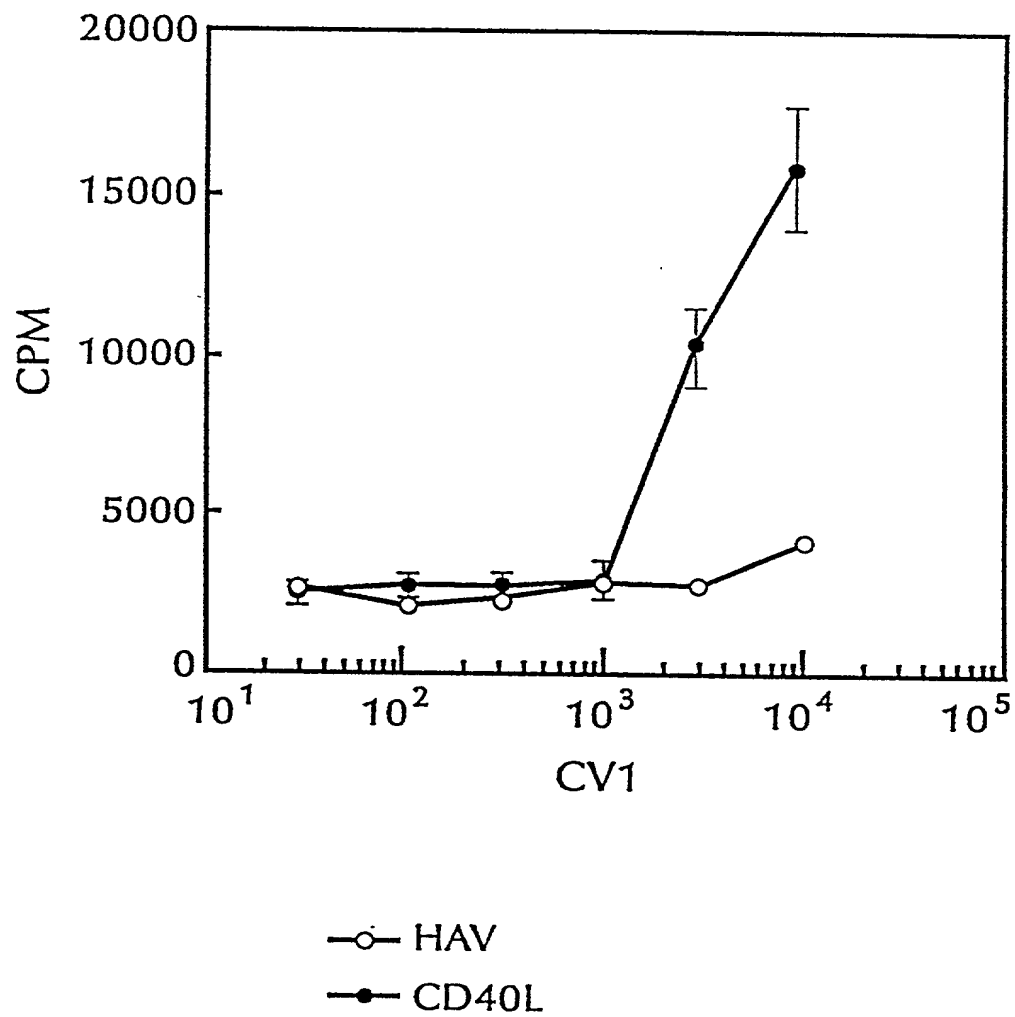


FIG. 6

S.CD23 in Day 6 Cultures S/N:
10E5 E-/Well, IMDM + IL-4

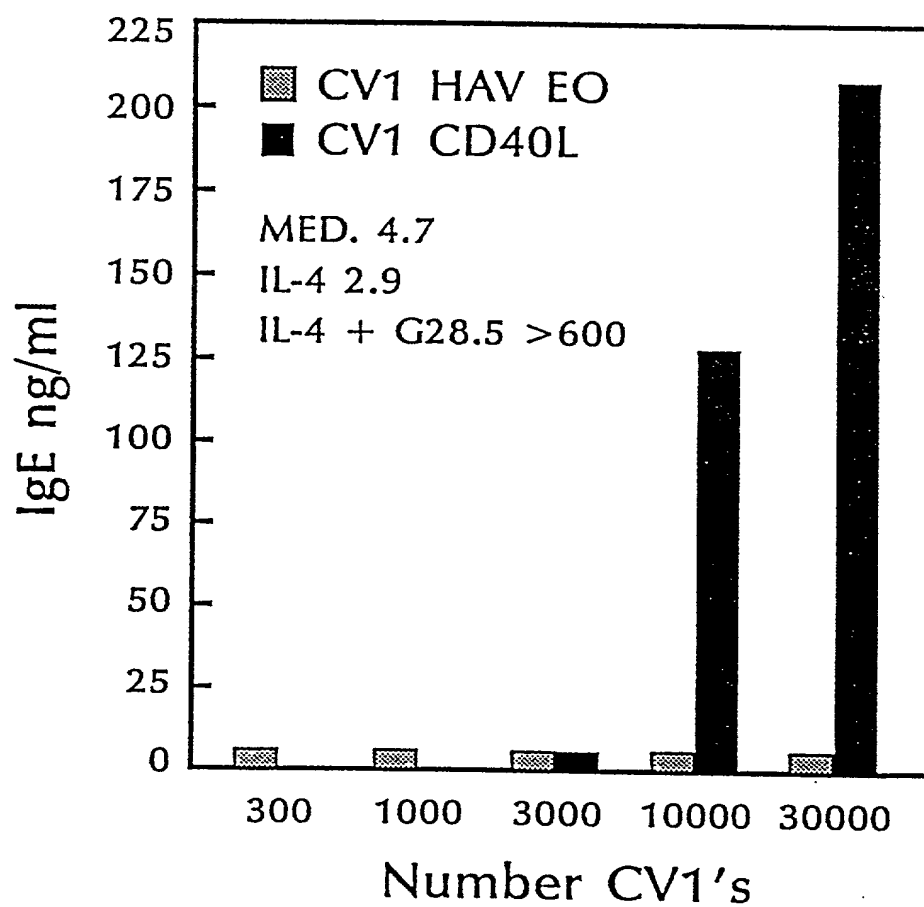


FIG. 7

S.CD23 in Day 6 Cultures S/N:
10E5 E-/Well, IMDM + IL-4

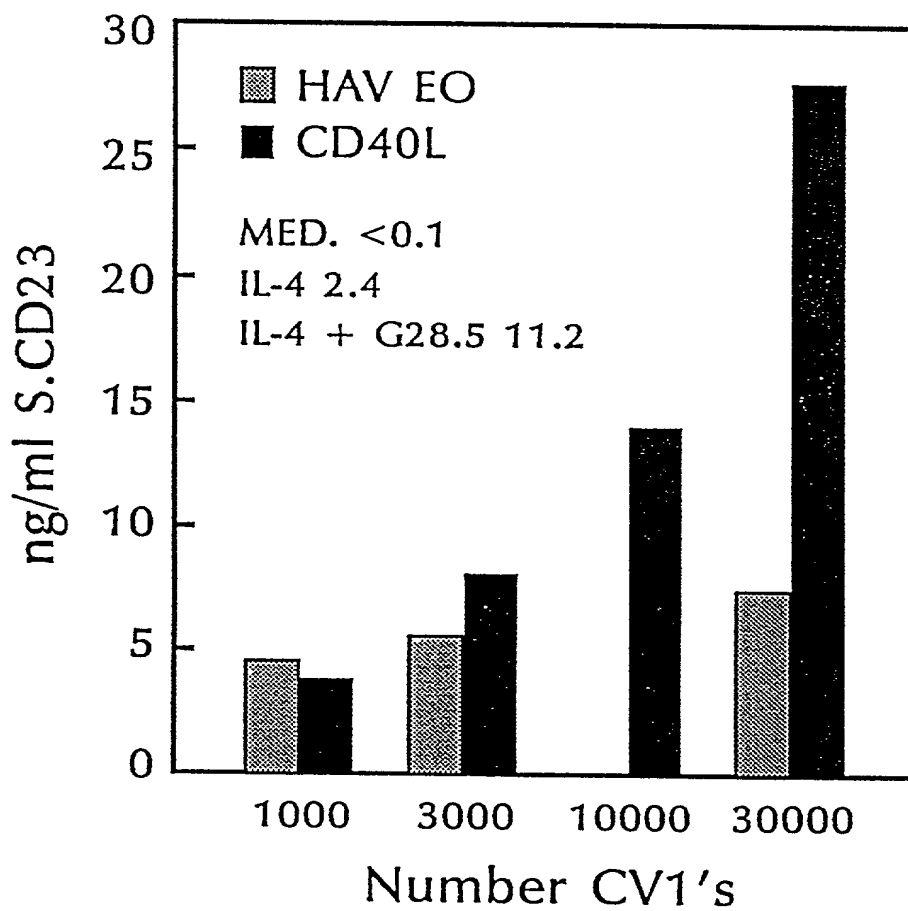
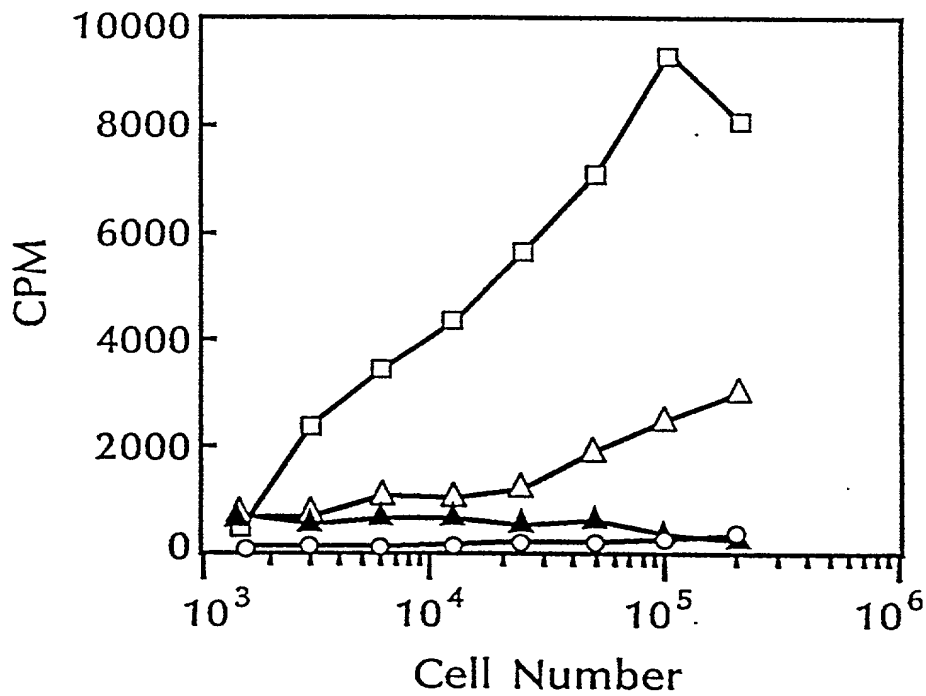


FIG. 8

Induction of B Cell Proliferation by
CD40 Ligand Expressing CV-1 Cells (fixed)



- CD40L
- △— 7A1
- ▲— HAV EO
- 40.9

FIG. 9

Induction of Anti-SRBC PFC by EL4 40.9
and 7A1 Th1 Cells (Fixed)

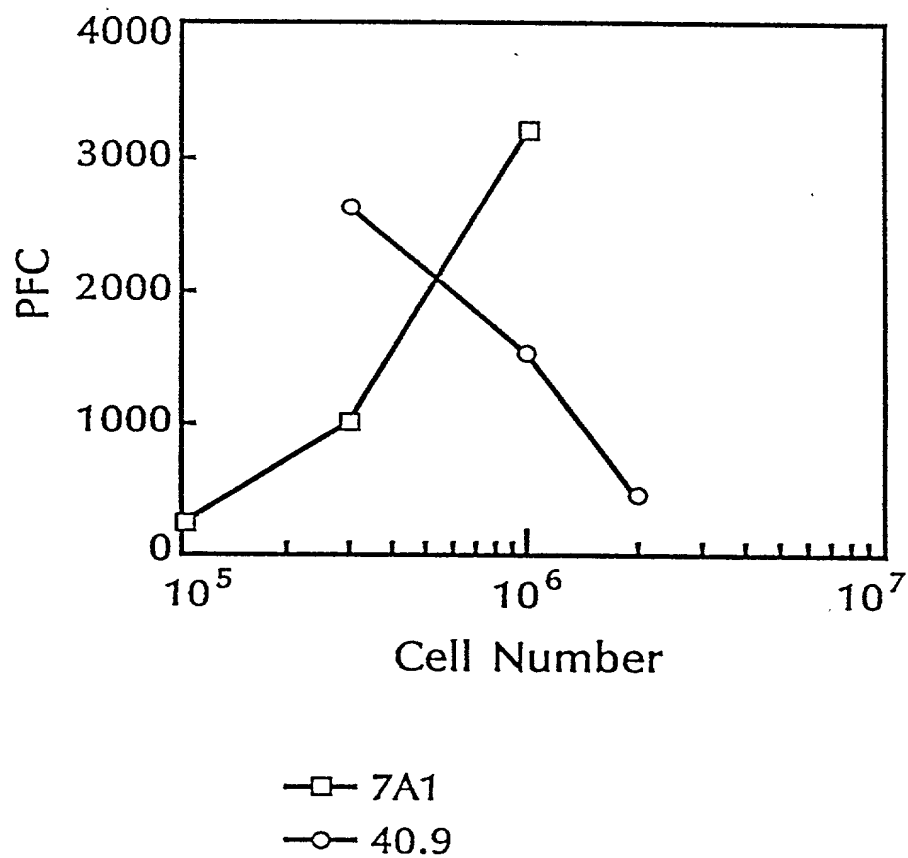
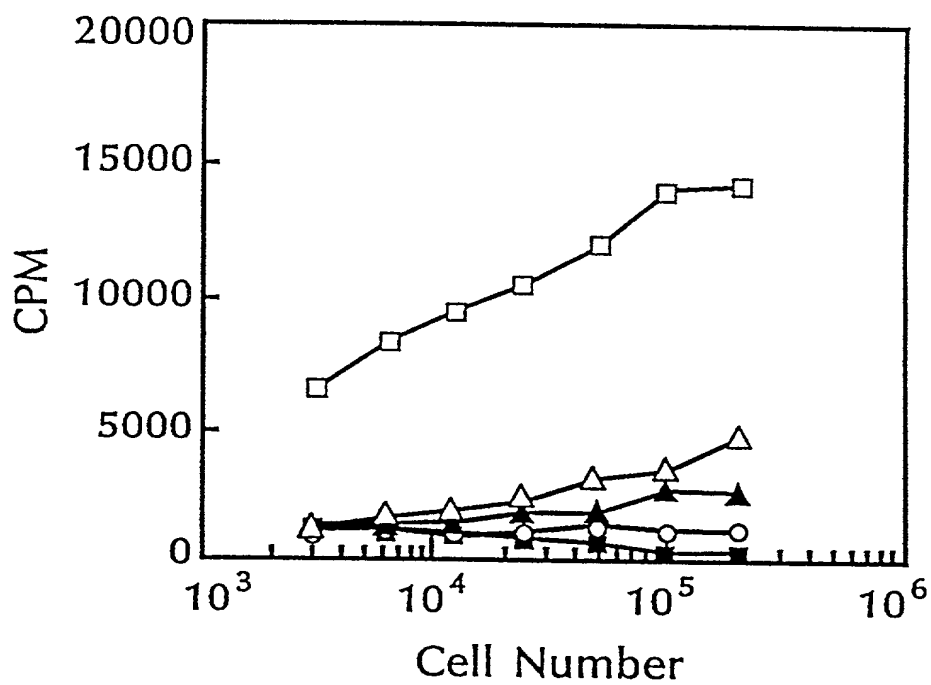


FIG. 10

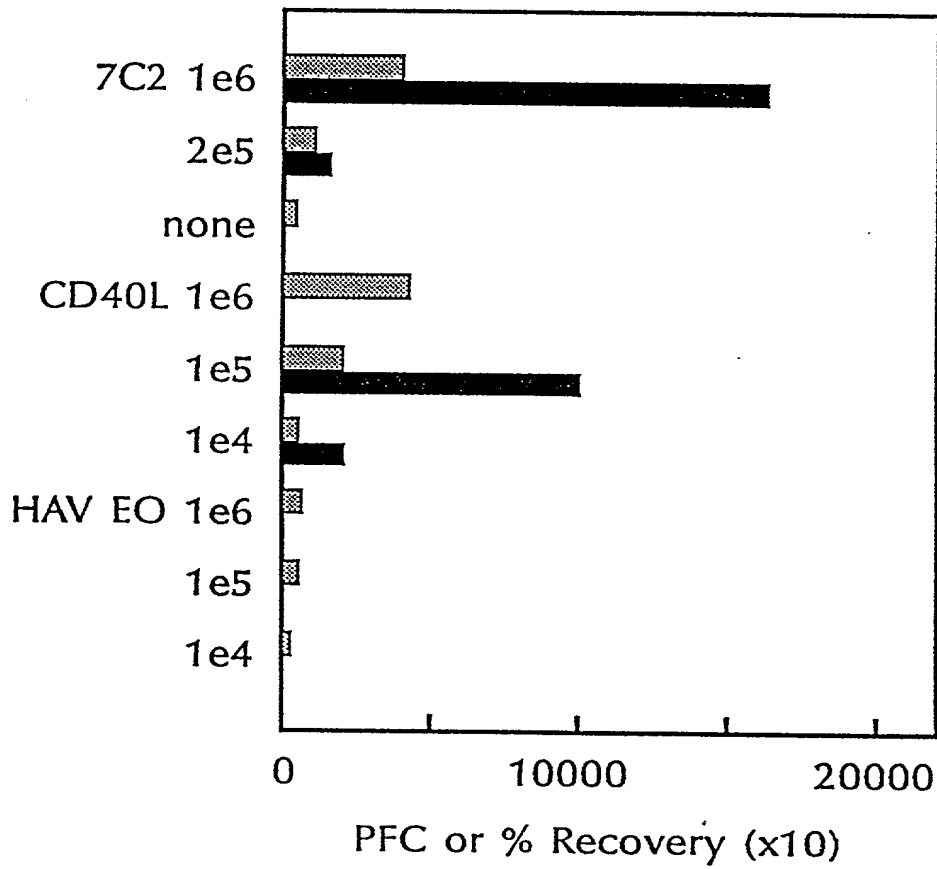
Induction of B Cell Proliferation by
CD40 Ligand Expressing CV-1 Cells



- CD40L
- △— 7A1
- HAV EO
- ▲— 7A1 + CD40Fc
- CD40Fc

FIG. 11

Induction of Anti-SRBC PFC by CD40
Ligand Expressing CV-1 Cells (fixed)



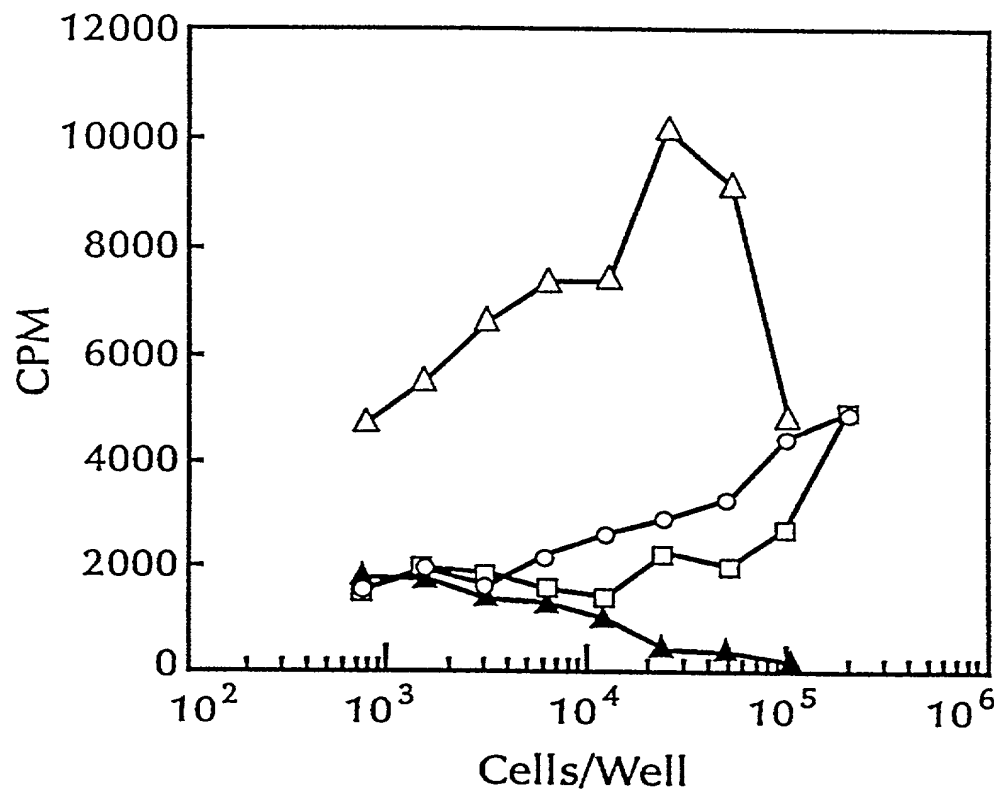
▨ % Recovery

■ PFC

3194-11

FIG. 12

Induction of Murine B Cell Proliferation by
CD40 Ligand Expressing CV-1 Cels (fixed)



- △— CD40L
- ▲— HAV EO
- 7C2 11/6
- 7A1 11/6

INDUCTION OF ANTIGEN SPECIFIC PFC BY
CD40 LIGAND EXPRESSING CV-1 CELLS (FIXED)

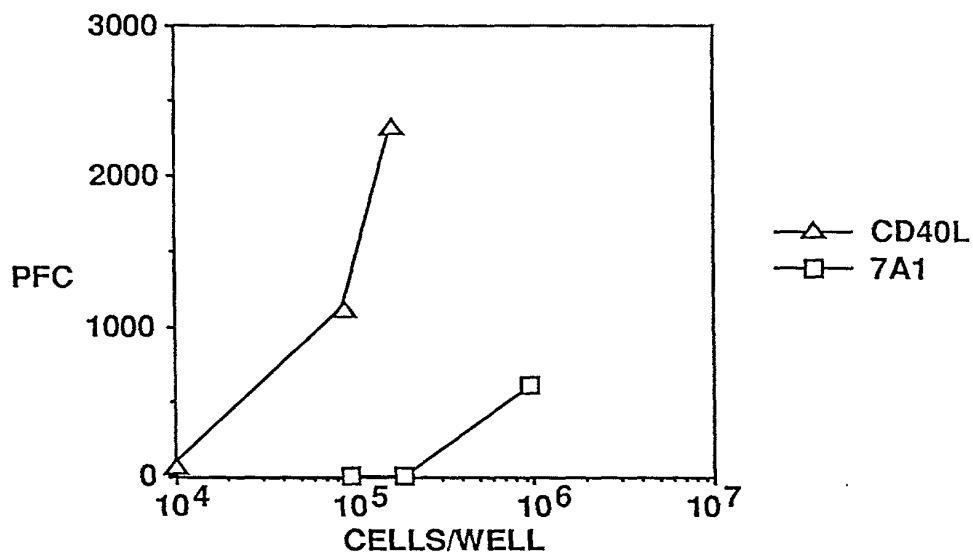


FIG. 13A

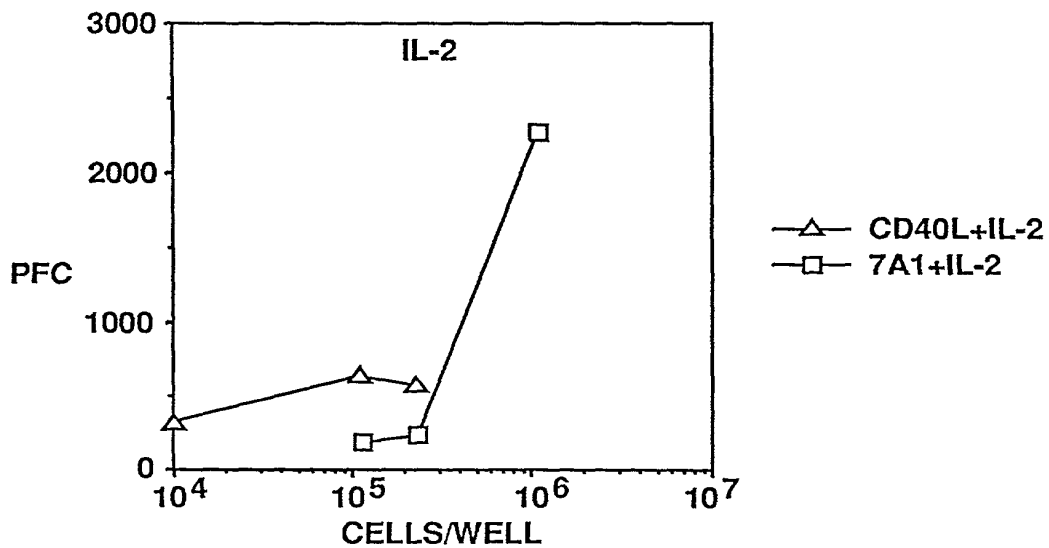


FIG. 13B

FIG. 14A

Day 7 Proliferation of T-depleted PBM

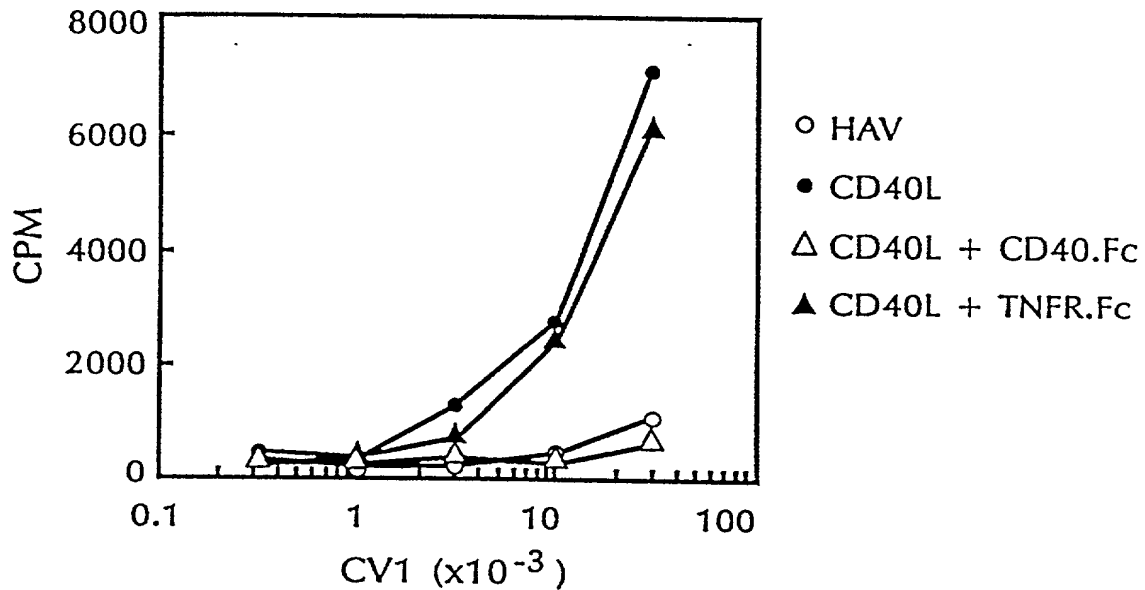


FIG. 14B

Day 10 IgE Secretion from T-depleted PBM

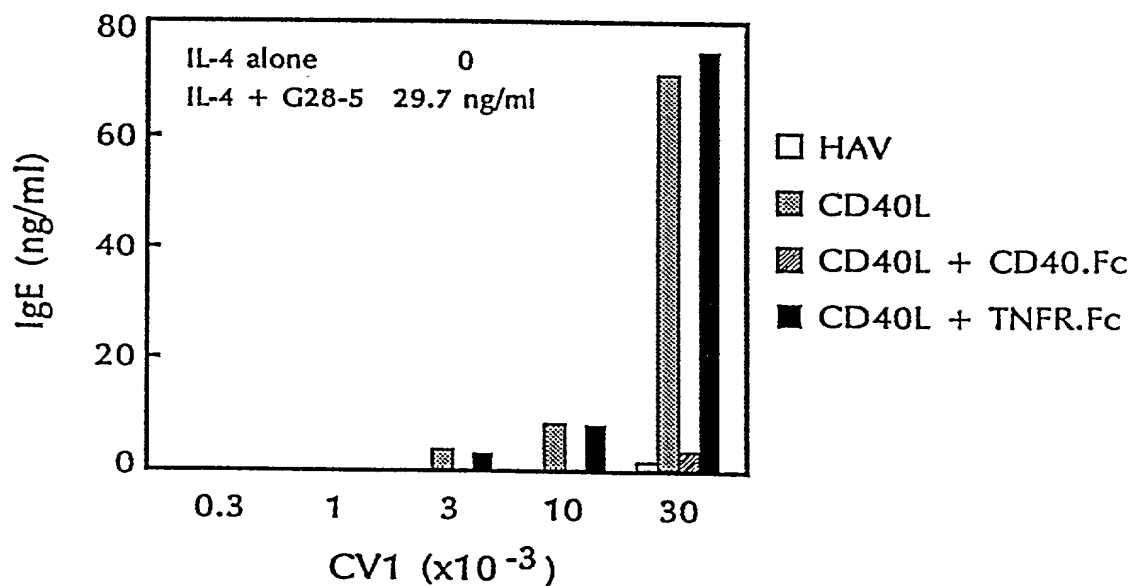


FIG. 15A

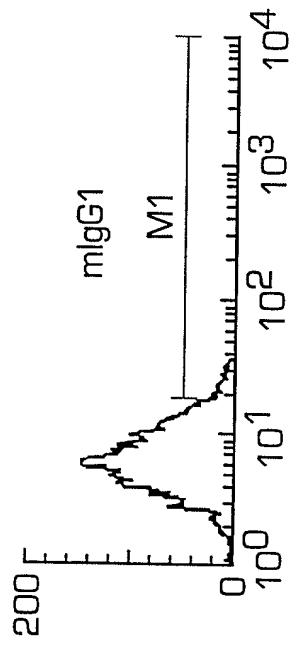


FIG. 15B

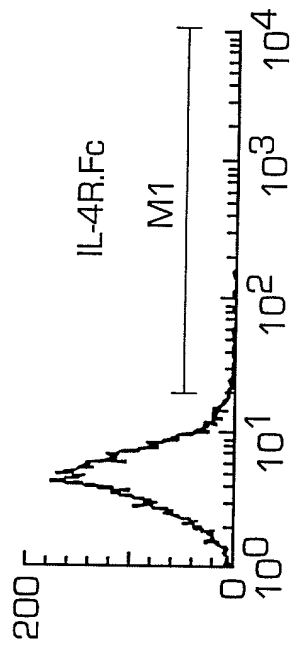


FIG. 15C

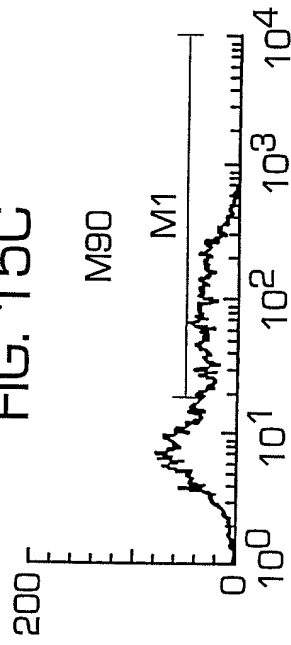
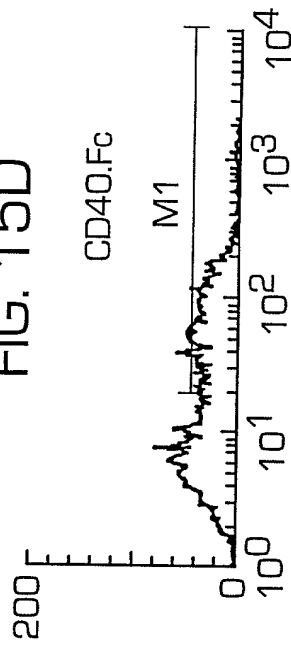


FIG. 15D



BINDING OF CD40.Fc AND ANTI-CD40L ANTIBODY M90
TO ACTIVATED PERIPHERAL BLOOD T CELLS

FIG. 16A

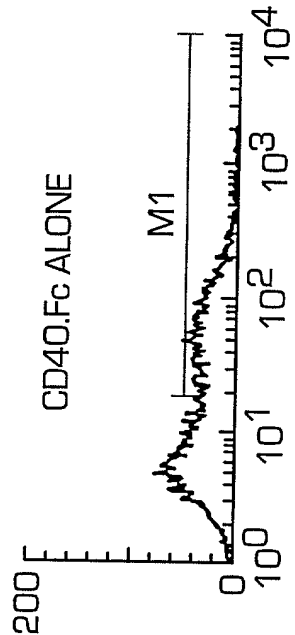


FIG. 16B

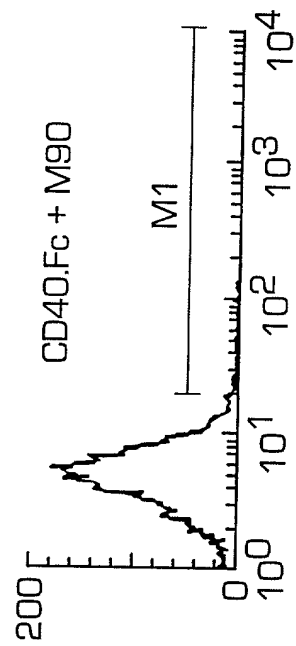


FIG. 16C

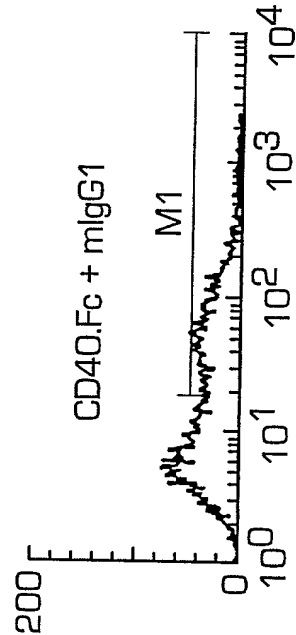
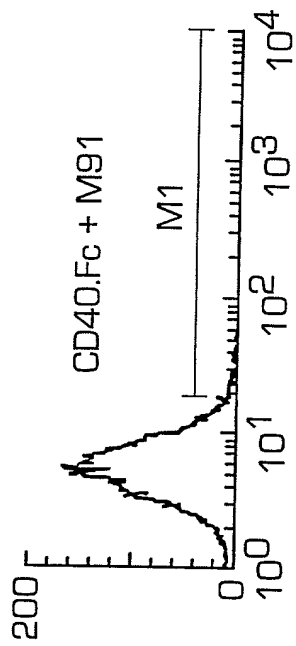


FIG. 16D



INHIBITION OF CD40.Fc BINDING TO ACTIVATED PERIPHERAL BLOOD T CELLS
BY ANTI-CD40L ANTIBODIES M90 AND M91

Inhibition of anti-IgM + soluble CD40L-induced
B-cell proliferation by anti-hCD40L mAb

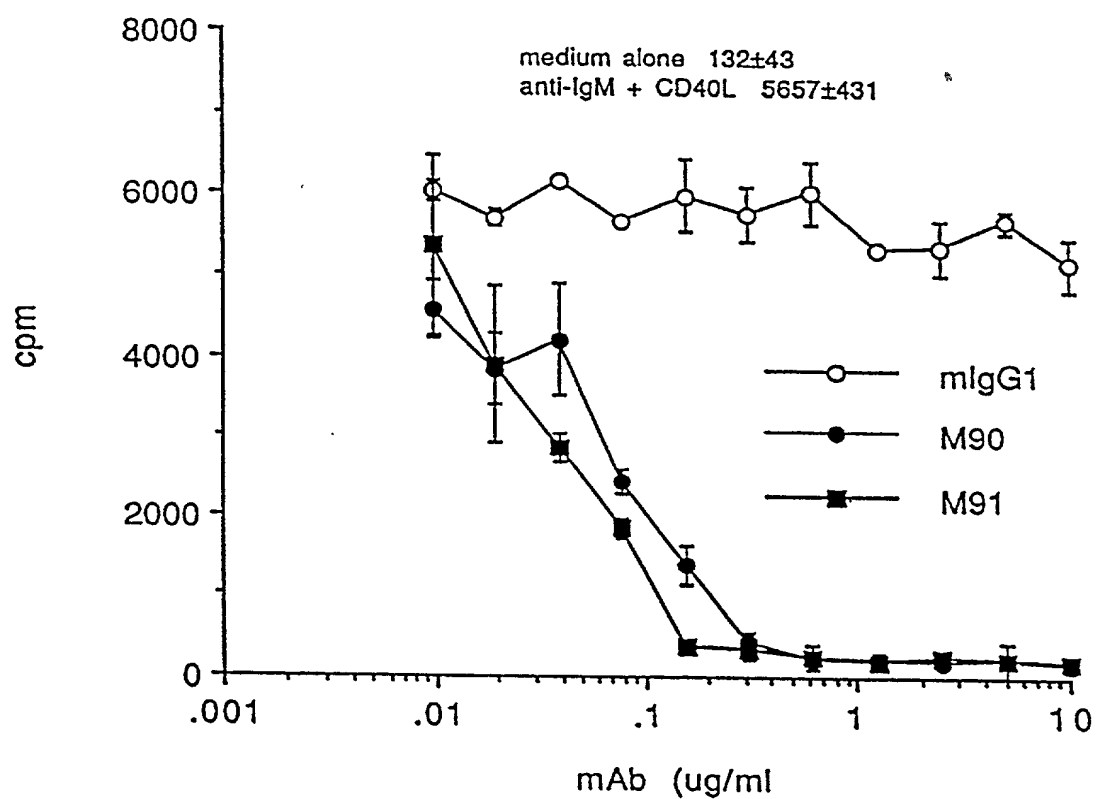


FIG. 17

Binding of human and Murine CD40 LT and CD40 L Fc
Dimer to CD40Fc by Biosensor Assay

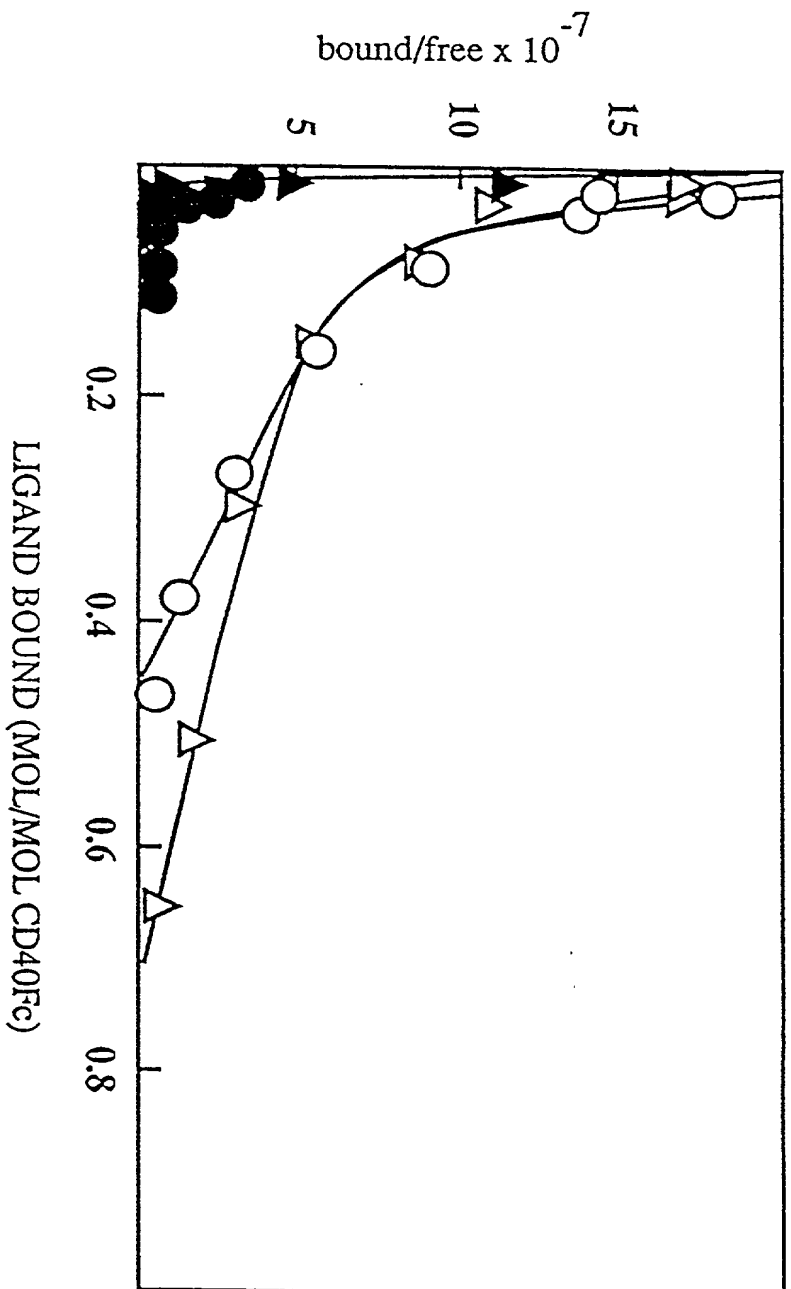


FIG. 18

FIG. 19A

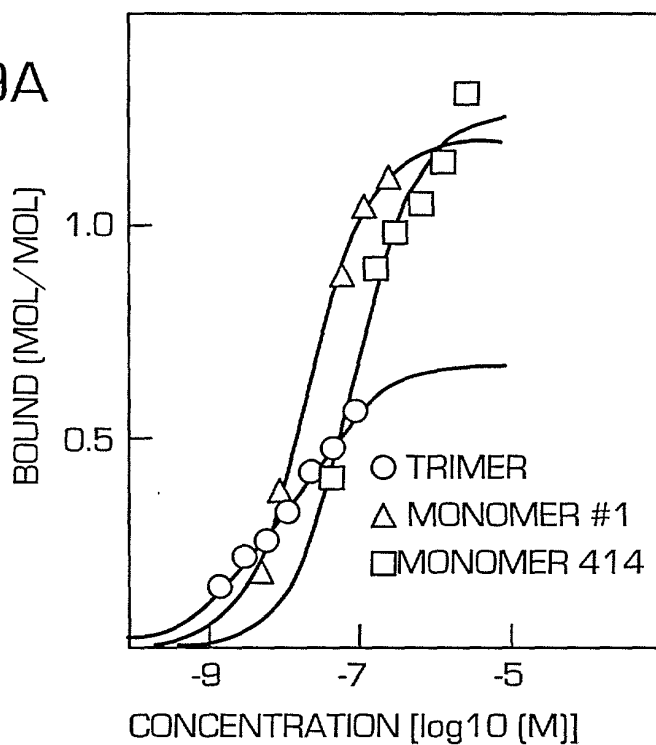
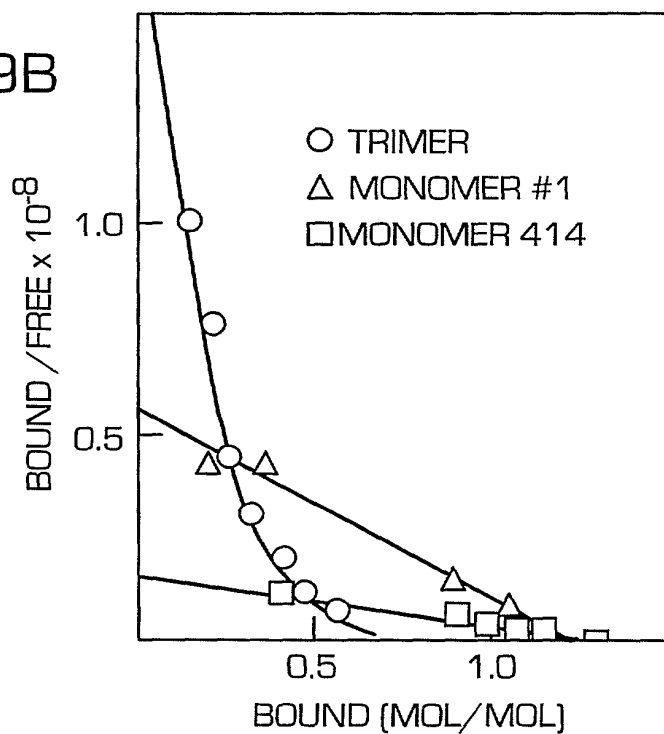


FIG. 19B



BINDING OF CD40 LIGANDS TO CD40Fc USING EQUILIBRIUM
BINDING VALUES ESTIMATED FROM A KINETIC ANALYSIS
OF THE ASSOCIATION PHASE

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of

RICHARD ARMITAGE et al

CONT. OF

Appln. No.: 08/249,189

Group Art Unit: 1644

Filed: May 28, 1999

Examiner: Gambel, P.

For: MONOCLONAL ANTIBODIES TO CD40 LIGAND
PHARMACEUTICAL COMPOSITION COMPRISING
THE SAME AND HYBRIDOMAS PRODUCING THE
SAME (As Amended)

STATEMENT IN SUPPORT OF SUBMISSION
IN ACCORDANCE WITH 37 C.F.R. § 1.821(e)

Assistant Commissioner
for Patents
Washington, D.C. 20231

Sir:

The following statement is provided to meet the requirements of 37 C.F.R. § 1.821(e).

I hereby state that the computer readable form of the Sequence Listing in the present application, i.e., Continuation of U.S. Appln. No. 08/249,189, is identical to that filed in Parent Application No. 08/249,189, filed May 24, 1994.

Further, in accordance with 37 C.F.R. § 1.821(e), please use the computer readable form of the Sequence Listing filed May 24, 1994, in the Parent Application as the computer readable form for the present application.

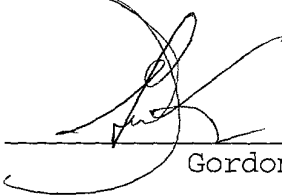
STATEMENT IN SUPPORT OF
SUBMISSION IN ACCORDANCE
WITH 37 C.F.R. § 1.821(e)
CONT. of USSN 08/249,189

It is understood that the U.S. Patent and Trademark Office will make the necessary changes in the application number and filing date for the computer readable form that will be used for the present application. Hence, a paper copy of the Sequence Listing filed in Parent Application No. 08/249,189 is submitted herewith for incorporation into the present specification.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge and that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

5/28/99

Date


Gordon Kit

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ARMITAGE, RICHARD
FANSLOW, WILLIAM
SPRIGGS, MELANIE
SRINIVASAN, SUBHASHINI
GIBSON, MARYLOU
- (ii) TITLE OF INVENTION: NOVEL CYTOKINE
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: IMMUNEX CORPORATION
 - (B) STREET: 51 UNIVERSITY STREET
 - (C) CITY: SEATTLE
 - (D) STATE: WASHINGTON
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Apple Operating System 7.1
 - (D) SOFTWARE: Microsoft Word for Apple, version 5.1a
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/969,703
 - (B) FILING DATE: October 23, 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/805,723
 - (B) FILING DATE: December 5, 1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/783,707
 - (B) FILING DATE: October 25, 1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Perkins, Patricia A.
 - (B) REGISTRATION NUMBER: 34,693
 - (C) REFERENCE/DOCKET NUMBER: 2802-C
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 2065870430
 - (B) TELEFAX: 2065870606

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MOUSE

(vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40-L

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA
48
Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
1 5 10 15
CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT
96
Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30
ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA
144
Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
35 40 45
AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA
192
Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
50 55 60
TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC
240
Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
65 70 75 80
TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG
288
Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
85 90 95

GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG
 336
 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
 100 105 110

CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA
 384
 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
 115 120 125

GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT
 432
 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
 130 135 140

TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG
 480
 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
 145 150 155 160

ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC
 528
 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
 165 170 175

TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC
 576
 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
 180 185 190

TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA
 624
 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
 195 200 205

AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG
 672
 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
 210 215 220

GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG
 720
 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
 225 230 235 240

ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC
 768
 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
 245 250 255

TTA CTC AAA CTC TGA
 783
 Leu Leu Lys Leu
 260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
1 5 10 15
Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30
Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
35 40 45
Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
50 55 60
Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
65 70 75 80
Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
85 90 95
Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
100 105 110
Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
115 120 125
Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
130 135 140
Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
145 150 155 160
Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
165 170 175
Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
180 185 190
Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
195 200 205
Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
210 215 220
Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
225 230 235 240
Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
245 250 255
Leu Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA
60

AAACTCACAC ATGCCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC
120

TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG
180

TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG
240

TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG
300

TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA
360

AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAA GCGAAAGGGC
420

AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG ACCAAGAACC
480

AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG
540

AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG
600

GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG
660

TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT
720

CCCTGTCTCC GGGTAAATGA
740

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGAACCACT CACTGCATGC AGAGAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT
60

TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC
120

TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC
180

ACAAATACTG CGACCCCAAC CTAGGGCTTC GGGTCCAGCA GAAGGGCACC TCAGAAACAG
240

ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG
300

TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGGTCAAGCA GATTGCTACA GGGGTTTCTG
360

ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA
420

AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA
480

ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA
519

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CD40 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGTCGACCA CCATGGTTCG TCTGCC
26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: CD40 3' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGTCGACGT CTAGAGCCGA TCCTGGGG
28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAGATCTG GGCTCTACGT ACTCAGCCGA TCCTGGGGAC
40

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PENTAPEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAAC CAC
43

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGGAGA CAGGGAGA
38

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40-L

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 46..831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCCACCTTC TCTGCCAGAA GATACCATTT CAACTTTAAC ACAGC ATG ATC GAA
54

Met Ile Glu
1

ACA TAC AAC CAA ACT TCT CCC CGA TCT GCG GCC ACT GGA CTG CCC ATC
102

Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly Leu Pro Ile
5 10 15

AGC ATG AAA ATT TTT ATG TAT TTA CTT ACT GTT TTT CTT ATC ACC CAG
150

Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln
20 25 30 35

ATG ATT GGG TCA GCA CTT TTT GCT GTG TAT CTT CAT AGA AGG TTG GAC
198

Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp
40 45 50

AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA
246

Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys
55 60 65

ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC
294

Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn
70 75 80

TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG
342

Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met
85 90 95

TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA
390

Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys
100 105 110 115

GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC
438

Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser
120 125 130

AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC
486

Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr
135 140 145

ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT
534

Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val
150 155 160

AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC
582

Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser
 165 170 175
 AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA
 630
 Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu
 180 185 190 195
 AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC
 678
 Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr
 200 205 210
 CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA
 726
 His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly
 215 220 225
 GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT
 774
 Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp
 230 235 240
 CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC
 822
 Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu
 245 250 255
 AAA CTC TGAACAGTGT CA
 840
 Lys Leu
 260

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
 1 5 10 15
 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30
 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
 35 40 45
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
 50 55 60
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser

| 65 | 70 | 75 | 80 |
|---|-----|-----|-----|
| Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys | 85 | 90 | 95 |
| Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu | 100 | 105 | 110 |
| Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser | 115 | 120 | 125 |
| Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly | 130 | 135 | 140 |
| Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln | 145 | 150 | 155 |
| Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr | 165 | 170 | 175 |
| Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser | 180 | 185 | 190 |
| Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala | 195 | 200 | 205 |
| Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His | 210 | 215 | 220 |
| Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn | 225 | 230 | 235 |
| Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe | 245 | 250 | 255 |
| Gly Leu Leu Lys Leu | 260 | | |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGTGGCGGA GGGTCAGGCG GAGGTGGGTC CGGAGGCGGG GGTTCAGTT CTGACAAGAT
60

AGAAGATGAA AGG
73

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCGCTCAG AGTTTGAGTA A
21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Human CD40-L/FC2 (soluble CD40-L)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1422

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 79..1422

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 4..78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAT ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG
48 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-25 -20 -15

ATC CTT GTT CTG CTG CCT GTC ACT AGC TCT GAC TAC AAA GAT GAC GAT
96 Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp
-10 -5 1 5

GAT AAA AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA
144 Asp Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
10 15 20

CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC
192 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
25 30 35

AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG
240 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
40 45 50

GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG
288 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
55 60 65 70

GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG
336 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
75 80 85

TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG
384 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
90 95 100

GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC
432 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
105 110 115

CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC
480 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
120 125 130

CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC
528 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
135 140 145 150

AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
 576
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 155 160 165

GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC
 624
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 170 175 180

AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC
 672
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 185 190 195

AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC
 720
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 200 205 210

TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC
 768
 Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 215 220 225 230

GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT
 816
 Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu
 235 240 245

CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA
 864
 His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly
 250 255 260

GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT
 912
 Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe
 265 270 275

GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA
 960
 Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys
 280 285 290

GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG
 1008
 Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala
 295 300 305 310

GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG
 1056
 Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln
 315 320 325

TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG
 1104
 Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu

| 330 | 335 | 340 |
|--|-----|-----|
| GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC 1152 | | |
| Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile 345 350 355 | | |
| TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT 1200 | | |
| Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala 360 365 370 | | |
| CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA 1248 | | |
| Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg 375 380 385 390 | | |
| ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG 1296 | | |
| Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly 395 400 405 | | |
| CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT 1344 | | |
| Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala 410 415 420 | | |
| TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT 1392 | | |
| Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr 425 430 435 | | |
| GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA 1425 | | |
| Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu 440 445 | | |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| |
|--|
| Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile -25 -20 -15 -10 |
| Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp -5 1 5 |
| Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 10 15 20 |

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 25 30 35
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 40 45 50 55
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 60 65 70
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 75 80 85
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 90 95 100
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 105 110 115
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 120 125 130 135
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 140 145 150
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 155 160 165
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 170 175 180
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 185 190 195
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 200 205 210 215
 Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 220 225 230
 Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu His
 235 240 245
 Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu
 250 255 260
 Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu
 265 270 275
 Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu
 280 285 290 295
 Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala
 300 305 310
 His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 315 320 325
 Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT
21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA
35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 929 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 65..142

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 65..886

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 143..886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC

| | |
|--|-----|
| CACC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG | 109 |
| Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu | |
| -26 -25 -20 -15 | |
| ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG AAA CAG ATA | 157 |
| Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile | |
| -10 -5 1 5 | |
| GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT ATA GAG AAT | 205 |
| Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn | |
| 10 15 20 | |
| GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT AGT TCT GAC | 253 |
| Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp | |
| 25 30 35 | |
| AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA | 301 |
| Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys | |
| 40 45 50 | |
| ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC | 349 |
| Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn | |
| 55 60 65 | |
| TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG | 397 |
| Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met | |
| 70 75 80 85 | |
| TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA | 445 |
| Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys | |
| 90 95 100 | |
| GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC | 493 |
| Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser | |
| 105 110 115 | |
| AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC | 541 |
| Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr | |
| 120 125 130 | |
| ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT | 589 |
| Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val | |
| 135 140 145 | |
| AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC | 637 |
| Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser | |
| 150 155 160 165 | |
| AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA | 685 |
| Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu | |
| 170 175 180 | |
| AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC | 733 |
| Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr | |
| 185 190 195 | |
| CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA | 781 |

| | | | | | | | | | | | | | | | | |
|-----|-----|------------|------------|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | Leu | Gly | Gly | |
| | | 200 | | | | | 205 | | | | | 210 | | | | |
| GTA | TTT | GAA | TTG | CAA | CCA | GGT | GCT | TCG | GTG | TTT | GTC | AAT | GTG | ACT | GAT | 829 |
| Val | Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | Val | Thr | Asp | |
| | 215 | | | | | 220 | | | | 225 | | | | | | |
| CCA | AGC | CAA | GTG | AGC | CAT | GGC | ACT | GGC | TTC | ACG | TCC | TTT | GGC | TTA | CTC | 877 |
| Pro | Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | Gly | Leu | Leu | |
| 230 | | | | | 235 | | | | 240 | | | | | 245 | | |
| AAA | CTC | TGAGCGGCCG | CTACAGATGA | ATAATAAGCA | TGTTTGGATT | CCTCAA | | | | | | | | | | 929 |
| Lys | Leu | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Phe | His | Val | Ser | Phe | Arg | Tyr | Ile | Phe | Gly | Ile | Pro | Pro | Leu | Ile | |
| -26 | -25 | | | | | -20 | | | | -15 | | | | | | |
| Leu | Val | Leu | Leu | Pro | Val | Thr | Ser | Ser | Asp | Arg | Met | Lys | Gln | Ile | Glu | |
| -10 | | | | | -5 | | | | | 1 | | | | 5 | | |
| Asp | Lys | Ile | Glu | Glu | Ile | Leu | Ser | Lys | Ile | Tyr | His | Ile | Glu | Asn | Glu | |
| | | | 10 | | | | | 15 | | | | | 20 | | | |
| Ile | Ala | Arg | Ile | Lys | Lys | Leu | Ile | Gly | Glu | Arg | Thr | Ser | Ser | Asp | Lys | |
| | 25 | | | | | 30 | | | | | 35 | | | | | |
| Ile | Glu | Asp | Glu | Arg | Asn | Leu | His | Glu | Asp | Phe | Val | Phe | Met | Lys | Thr | |
| | 40 | | | | | 45 | | | | 50 | | | | | | |
| Ile | Gln | Arg | Cys | Asn | Thr | Gly | Glu | Arg | Ser | Leu | Ser | Leu | Leu | Asn | Cys | |
| 55 | | | | | 60 | | | | | 65 | | | | 70 | | |
| Glu | Glu | Ile | Lys | Ser | Gln | Phe | Glu | Gly | Phe | Val | Lys | Asp | Ile | Met | Leu | |
| | | | | 75 | | | | 80 | | | | | 85 | | | |
| Asn | Lys | Glu | Glu | Thr | Lys | Lys | Glu | Asn | Ser | Phe | Glu | Met | Gln | Lys | Gly | |
| | | 90 | | | | | | 95 | | | | | 100 | | | |
| Asp | Gln | Asn | Pro | Gln | Ile | Ala | Ala | His | Val | Ile | Ser | Glu | Ala | Ser | Ser | |
| | 105 | | | | | 110 | | | | | 115 | | | | | |
| Lys | Thr | Thr | Ser | Val | Leu | Gln | Trp | Ala | Glu | Lys | Gly | Tyr | Tyr | Thr | Met | |
| 120 | | | | | | 125 | | | | | 130 | | | | | |
| Ser | Asn | Asn | Leu | Val | Thr | Leu | Glu | Asn | Gly | Lys | Gln | Leu | Thr | Val | Lys | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 135 | | 140 | | 145 | | 150 | | | | | | | | | |
| Arg | Gln | Gly | Leu | Tyr | Tyr | Ile | Tyr | Ala | Gln | Val | Thr | Phe | Cys | Ser | Asn |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Arg | Glu | Ala | Ser | Ser | Gln | Ala | Pro | Phe | Ile | Ala | Ser | Leu | Cys | Leu | Lys |
| | | | 170 | | | | | 175 | | | | | 180 | | |
| Ser | Pro | Gly | Arg | Phe | Glu | Arg | Ile | Leu | Leu | Arg | Ala | Ala | Asn | Thr | His |
| | | 185 | | | | | 190 | | | | | 195 | | | |
| Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | Leu | Gly | Gly | Val |
| | | 200 | | | | 205 | | | | | 210 | | | | |
| Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | Val | Thr | Asp | Pro |
| 215 | | | | | 220 | | | | | 225 | | | | | 230 |
| Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | Gly | Leu | Leu | Lys |
| | | | | 235 | | | | | 240 | | | | | 245 | |

Leu

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (B) CLONE: Murine CD40-L trimer

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 15..92

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..857

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | | | | | | | | | | |
|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTCGAGGTAC | CGCC | ATG | TTC | CAT | GTT | TCT | TTT | AGA | TAT | ATC | TTT | GGA | ATT | 50 | |
| | | Met | Phe | His | Val | Ser | Phe | Arg | Tyr | Ile | Phe | Gly | Ile | | |
| | | -26 | -25 | | | | | -20 | | | | -15 | | | |
| CCT | CCA | CTG | ATC | CTT | GTT | CTG | CTG | CCT | GTC | ACT | AGT | TCT | GAC | CGT | ATG |
| Pro | Pro | Leu | Ile | Leu | Val | Leu | Leu | Pro | Val | Thr | Ser | Ser | Asp | Arg | Met |
| | | | | -10 | | | | -5 | | | | | | 1 | |

| | |
|---|-----|
| AAA CAG ATA GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT | 146 |
| Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His | |
| 5 10 15 | |
| ATA GAG AAT GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT | 194 |
| Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr | |
| 20 25 30 | |
| AGT TCT GAC TAC AAA GAT GAC GAT GAT AAA GAT AAG GTC GAA GAG GAA | 242 |
| Ser Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu | |
| 35 40 45 50 | |
| GTA AAC CTT CAT GAA GAT TTT GTA TTC ATA AAA AAG CTA AAG AGA TGC | 290 |
| Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys | |
| 55 60 65 | |
| AAC AAA GGA GAA GGA TCT TTA TCC TTG CTG AAC TGT GAG GAG ATG AGA | 338 |
| Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg | |
| 70 75 80 | |
| AGG CAA TTT GAA GAC CTT GTC AAG GAT ATA ACG TTA AAC AAA GAA GAG | 386 |
| Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu | |
| 85 90 95 | |
| AAA AAA GAA AAC AGC TTT GAA ATG CAA AGA GGT GAT GAG GAT CCT CAA | 434 |
| Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln | |
| 100 105 110 | |
| ATT GCA GCA CAC GTT GTA AGC GAA GCC AAC AGT AAT GCA GCA TCC GTT | 482 |
| Ile Ala Ala His Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val | |
| 115 120 125 130 | |
| CTA CAG TGG GCC AAG AAA GGA TAT TAT ACC ATG AAA AGC AAC TTG GTA | 530 |
| Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val | |
| 135 140 145 | |
| ATG CTT GAA AAT GGG AAA CAG CTG ACG GTT AAA AGA GAA GGA CTC TAT | 578 |
| Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr | |
| 150 155 160 | |
| TAT GTC TAC ACT CAA GTC ACC TTC TGC TCT AAT CGG GAG CCT TCG AGT | 626 |
| Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser | |
| 165 170 175 | |
| CAA CGC CCA TTC ATC GTC GGC CTC TGG CTG AAG CCC AGC AGT GGA TCT | 674 |
| Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser | |
| 180 185 190 | |
| GAG AGA ATC TTA CTC AAG GCG GCA AAT ACC CAC AGT TCC TCC CAG CTT | 722 |
| Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu | |
| 195 200 205 210 | |
| TGC GAG CAG CAG TCT GTT CAC TTG GGC GGA GTG TTT GAA TTA CAA GCT | 770 |
| Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala | |
| 215 220 225 | |
| GGT GCT TCT GTG TTT GTC AAC GTG ACT GAA GCA AGC CAA GTG ATC CAC | 818 |

Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His
 230 235 240

AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC
 Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
 245 250 255

864

CGCTACAGAT CTAC

878

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
 -26 -25 -20 -15

Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
 -10 -5 1 5

Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu
 10 15 20

Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp Tyr
 25 30 35

Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu Val Asn Leu His
 40 45 50

Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu
 55 60 65 70

Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu
 75 80 85

Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn
 90 95 100

Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His
 105 110 115

Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala
 120 125 130

Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn
 135 140 145 150

Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr
 155 160 165

Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe

| 170 | | | | | | | 175 | | | | | 180 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Val | Gly | Leu | Trp | Leu | Lys | Pro | Ser | Ser | Gly | Ser | Glu | Arg | Ile | Leu | |
| | | 185 | | | | | 190 | | | | | 195 | | | | |
| Leu | Lys | Ala | Ala | Asn | Thr | His | Ser | Ser | Ser | Gln | Leu | Cys | Glu | Gln | Gln | |
| | 200 | | | | | 205 | | | | | 210 | | | | | |
| Ser | Val | His | Leu | Gly | Gly | Val | Phe | Glu | Leu | Gln | Ala | Gly | Ala | Ser | Val | |
| 215 | | | | | 220 | | | | | 225 | | | | | 230 | |
| Phe | Val | Asn | Val | Thr | Glu | Ala | Ser | Gln | Val | Ile | His | Arg | Val | Gly | Phe | |
| | | | | 235 | | | | | 240 | | | | | 245 | | |
| Ser | Ser | Phe | Gly | Leu | Leu | Lys | Leu | | | | | | | | | |
| | | | 250 | | | | | | | | | | | | | |